

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	43	14.8	10968	12	US-11-075-185-35	Sequence 35, Appl
2	43	14.8	78869	12	US-11-075-185-1	Sequence 1, Appl
3	41.4	14.2	874	9	US-11-177-506-23	Sequence 23, Appl
4	40.2	13.8	730	8	US-10-750-185-623340	Sequence 62340, A
5	40.2	13.8	730	8	US-10-750-623-62340	Sequence 62340, A
6	40	13.7	2886	8	US-10-504-599A-15	Sequence 15, Appl
7	39.2	13.5	1000	12	US-11-000-688-1411	Sequence 1411, Ap
8	38.6	13.3	1962	8	US-10-821-234-434	Sequence 434, App
9	38	13.1	720	11	US-11-079-906-1	Sequence 1, Appl
10	38	13.1	720	11	US-11-079-476-1	Sequence 1, Appl
11	38	13.1	725	12	US-11-170-693-70	Sequence 70, Appl
12	38	13.1	726	12	US-11-175-690-115	Sequence 115, App
13	38	13.1	1314	12	US-11-069-642-46	Sequence 46, Appl
14	38	13.1	1314	12	US-11-069-642-48	Sequence 48, Appl
15	38	13.1	1314	12	US-11-069-643-50	Sequence 50, Appl
16	38	13.1	1314	12	US-11-069-642-52	Sequence 52, Appl
17	38	13.1	1314	12	US-11-069-642-54	Sequence 54, Appl
18	38	13.1	1314	12	US-11-069-642-56	Sequence 56, Appl
19	38	13.1	1314	12	US-11-069-643-58	Sequence 58, Appl
20	38	13.1	1314	12	US-11-069-643-60	Sequence 60, Appl

RESULT 2

US-11-075-185-1
; Sequence 1, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1

Query Match 14.8%; Score 43; DB 12; Length 78869;
Best Local Similarity 48.9%; Pred. No. 0.027;
Matches 115; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
Qy 39 GAAGACGCTGGTGTGAACATCAAGTACAGAGGCCAGGGGACACCCCTGGCGGAGGTGGA 98
Db 16440 GATGAAGCTGGTGTGGCGATGACGACGACGAGAGCTGCCAGGAGCGCTGCACGCCGACCC 16499
Qy 99 GCTCCGCGACGCGCTCGGAGGAGTGGAAACCCATGACGAAGAGGCAACCTGTGGGA 158
Db 16500 GCCCTCGCGCGACGCTGCACTGGTGGCGGACGTCAGCTCTGAAAGAGCCGCTGCC 16559
Qy 159 GGTGAAGAGCCCAAGCGCTCACCGGCCCAATGAACCTTCGCTTCTTCAAGGGCGG 218
Db 16560 GTGCGCGCGACGAGCCGCGCGCGCGCGCGCTCTCGCTTTCAGCGGCGAC 16619
Qy 219 CATGAAGAACGCTTTCGACGAGGTTCATCCCGCCGCTTTCAGGTGCGCAAAACC 273
Db 16620 CAACGCGACGTCATCGTTCGAGAGGCGCGCGCGCGCTTCCACCGAGGCGACGACC 16674

RESULT 3

US-11-177-506-23
; Sequence 23, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blaesius, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)...(702)
US-11-177-506-23

Query Match 14.2%; Score 41.4; DB 9; Length 874;
Best Local Similarity 51.3%; Pred. No. 0.056;
Matches 96; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
Qy 62 AGTACACGAGGCCAGGGGACACCCCTGGCGGAGGTGGAGTCCGGCAGCAGCGGTTCGAGG 121
Db 230 AGCTCAAGAGCGCTCTGGACACCCCTGGCCAGGAGGTGGCCCTGTCTGAAGAGCAGCAGG 289
Qy 122 AGTGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGGCCCAAGCCGCTCA 181
Db 290 CCCTGCAGACGGTCTGCCTGAAGGGGACCAAGGTGCACATGAATGCTTTCTGGCCTTCA 349
Qy 182 CCGGCCCAATGAATTCGGCTTCTTCAAGGGCGGCATGAAGAAGCTCTTCGACGAGG 241
Db 350 CCCAGACGAAGACCTTCCACGAGGCCAGCGAGGACTGCATCTCGCGCGGGGACACCTGA 409
Qy 242 TCATCCC 248
Db 410 GCACCCC 416

RESULT 4

US-10-750-185-62340
; Sequence 62340, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62340
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-62340

Query Match 13.8%; Score 40.2; DB 8; Length 730;
Best Local Similarity 55.3%; Pred. No. 0.12;
Matches 78; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 20 TGGAGAAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAAGTACACGAGGCCAGGG 79
Db 433 TGGAGAGGAGGGCGAGCTGCAGAGGCTGCACCGCAGCTTCGAGAGAAGAGCTGGCGG 492
Qy 80 ACACCTTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGAGTGGGAACCCATGAGA 139
Db 493 CCAGCAACCTTACGAGGAGCGCGCGCGCTCTCAAGGACGAGCTGGAGGGCTGGAGG 552
Qy 140 ARAAGGGCAACCTGTGGGAGG 160
Db 553 CCAAGGGCAAGTGAAGGTGG 573

RESULT 5

US-10-750-623-62340
; Sequence 62340, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
US-10-750-623-62340

APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62340
LENGTH: 730
TYPE: DNA
ORGANISM: Bovine 19866881552925
US-10-750-623-62340

Query Match 13.8%; Score 40.2; DB 8; Length 730;
Best Local Similarity 55.3%; Pred. No. 0.12;
Matches 78; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 20 TGGAGAGGGTTCTGACGGAGAGCGCTGGTCTGAACATCAAGTACACGAGGCCACGGG 79
DB 433 TGGAGAGGGGGCGGAGCTGCAGAGCTGCACCGAGCTTCGAGGAGAGGAGCTGGCG 492

QY 80 ACACCTTGGCGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGAGTGGGAACCCATGACGA 139
DB 493 CCAGCCACCTTACGAGAGCGCGCGCGCTGCNAAGCAGGCTGGAGGGGCTGGAGG 552

QY 140 AGAAGGGCAACTGTGGGAGG 160
DB 553 CCAAGGCAAGATGAAGGTGG 573

RESULT 6

US-10-504-599A-15
Sequence 15, Application US/10504599A
Publication No. US20050272033A1
GENERAL INFORMATION:
APPLICANT: YAMAKAWA, HIROHITO
APPLICANT: SUZUKI, ERIKO
APPLICANT: MIYATAKE, KIYOKO
APPLICANT: HAYAKAWA, KATSUYUKI
TITLE OF INVENTION: WHEAT DETECTING METHOD
FILE REFERENCE: 8036-1018
CURRENT APPLICATION NUMBER: US/10/504,599A
CURRENT FILING DATE: 2004-08-16
PRIOR APPLICATION NUMBER: PCT/JP02/09983
PRIOR FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: JP 2002-39040
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: JP 2002-132119
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 15
LENGTH: 2886
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-504-599A-15

Query Match 13.7%; Score 40; DB 8; Length 2886;
Best Local Similarity 47.6%; Pred. No. 0.14;
Matches 118; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 26 AGGGTTCTGACCGAAGACGCTGGTCTGAACATCAAGTACACGAGGCCGGGACACCC 85
DB 1457 ACGGCTACGACAAAGCGGTGGAGGGCGCAAGATCACTGGATGAAGCCGGGATCCTGC 1516

QY 86 TGGCGGAGGTGAGCTCCGGGAGCAGCGGCTCGGAGAGTGGGAACCCATGACGAAGAG 145
DB 1517 AGGCCGCAAGGTGTGAGGTGAGCCCTACTACGCGGAGGAGCTCATCTCTGCGGAAG 1576

QY 146 GCAACCTGTGGAGGTGAAGAGCGCAAGCGCTCACCGGCCCAATGAATCTTCGGCTTCC 205
DB 1577 CCAGGGGCTGCGAGCTCGACACATCATGTGGCTCACTGGGATCACCGGCATCGTCAACG 1636

QY 206 TCTCAAGGGCGGCATGAAGAAGCTTTCGACGAGGTATCCCGACCGCTTCACGGTGC 265
DB 1637 GCATGGATGTTAGCGAGTGGGACCCCAAGGACAAGTTCTCGCGCTCAACTACGACA 1696

QY 266 GCAAAACC 273
DB 1697 TCACCACC 1704

RESULT 7

US-11-000-688-1411
Sequence 1411, Application US/11000688
Publication No. US20050287544A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, Francois
APPLICANT: HOULGATTE, Remi
APPLICANT: BIRNBAUM, Daniel
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILE REFERENCE: 1423-R-03
CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT FILING DATE: 2004-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
PRIOR FILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1411
LENGTH: 1000
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequences:primer
NAME/KEY: misc feature
LOCATION: (1)..(1000)
OTHER INFORMATION: troponin t3, skeletal, fast(TNNT3) gene.
US-11-000-688-1411

Query Match 13.5%; Score 39.2; DB 12; Length 1000;
Best Local Similarity 49.1%; Pred. No. 0.22;
Matches 104; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 20 TGGAGAGGGTTCTGACCGGAAGAGCGCTGGTGTCTGAACATCAAGTACACGAGGCCACGGG 79
DB 299 TCGAAGAGCGCGGTGTCAGAGAGAGCGGAGCAGAGGATTGCTGCAGAGAGGAGAGG 358

QY 80 ACACCTTGGCGAGGTGGAGCTCCGGCAGCAGCGCTCCGAGGAGTGGGAACCCATGACGA 139
DB 359 AGCGCCAGACAGACTGCGGAGGAGGAGGAGGAGGAGGAGGATGCAAGAGGA 418

QY 140 AGAAGGGCAACTGTGGAGGTGAAGAGCGCCCAAGCCGCTCACCGGCCCAATGAATCTTC 199
DB 419 GGGCAGAGGACGACCTGAAGAAGAAAGCGCTGCTCTCCATGGCGCGCAACTACGACA 478

QY 200 GCTTCTCTCCAGGGCGGCATGAAGAAGCTC 231
DB 479 GCTACTGCGCAAGGCTGACCAGAGAGAGGC 510

RESULT 8

US-10-821-234-434
Sequence 434, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 434
LENGTH: 1962
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-434

Query Match 13.3%; Score 38.6; DB 8; Length 1962;
Best Local Similarity 49.3%; Pred. No. 0.34;
Matches 101; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 81 CACCCTGCGGAGGTGGAGCTCCGCGCAGCAGCGCTCGGAGGAGTGGGAACCCATGACGAA 140
DB 9 CTCCTGTGTGCGCGATGCTGCTGCTGCTCAGCGCGCGCGCGCGGAGGAGGACAA 68
QY 141 GAAGGGCAACCTGTGGGAGGTGAAGCGCCAGCGCTCACCGGCCCAATGAATTCGG 200
DB 69 GAAGGAGACGTGGGCACGGTGGTGGCATCGACTTGGGGACCACTACTCTCTGCTCGG 128
QY 201 CTTCTCTCCAAAGGCGGCATGAGAACTGTTCCAGCAGGTCTATCCCCACCGCTTCAC 260
DB 129 CGTGTTCAGAACACGCGCGGTGGAGATCATCGCAACGATCAGGGCAACCGCATCACGC 188
QY 261 GGTCCGCAAAACCTACACCCAGAA 285
DB 189 GTCCTATGTCGCTTCACTCTCTGAA 213

RESULT 9
US-11-079-906-1
Sequence 1, Application US/11079906
Publication No. US20050244858A1
GENERAL INFORMATION:
APPLICANT: City of Hope
APPLICANT: Integrated DNA Technologies
APPLICANT: Rossi, John J.
APPLICANT: Behlke, Mark A.
APPLICANT: Kim, Dongho
TITLE OF INVENTION: Methods and Compositions for the Specific Inhibition of Gene
FILE REFERENCE: 1954-434
CURRENT APPLICATION NUMBER: US/11/079,906
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 60/553,487
PRIOR FILING DATE: 2004-03-15
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: EGFP from cloning vector pEGFP-C1
US-11-079-906-1

Query Match 13.1%; Score 38; DB 11; Length 720;
Best Local Similarity 57.6%; Pred. No. 0.46;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAGAGCGCCAAAGCGCTCACCGGCCCAATGAATTCCTTCCAAAGGCGCGC 219
DB 205 GTGAGTGTTCAGCGCTACCCGACACATGAAGCAGCAGCTTCTTCAAGTCGCGC 264
QY 220 ATGAAGAAGCTTTGACAGGTCTATCCCAAGCGCTTCCAGTGGGCAAACTTACA 277
DB 265 ATGCCGGAAGGTAGCTCCAGGAGCGCACCATCTTCTTCAAGGACGACGCGCACTACA 322

RESULT 10
US-11-079-476-1
Sequence 1, Application US/11079476
Publication No. US20050277610A1
GENERAL INFORMATION:
APPLICANT: City of Hope
APPLICANT: Integrated DNA Technologies
APPLICANT: Rossi, John J.
APPLICANT: Behlke, Mark A.
APPLICANT: Kim, Dongho
TITLE OF INVENTION: Methods and Compositions for the Specific Inhibition of Gene
FILE REFERENCE: 1954-463
CURRENT APPLICATION NUMBER: US/11/079,476
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 60/553,487
PRIOR FILING DATE: 2004-03-15
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: EGFP from cloning vector pEGFP-C1
US-11-079-476-1

Query Match 13.1%; Score 38; DB 12; Length 720;
Best Local Similarity 57.6%; Pred. No. 0.46;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAGAGCGCCAAAGCGCTCACCGGCCCAATGAATTCCTTCCAAAGGCGCGC 219
DB 205 GTGAGTGTTCAGCGCTACCCGACACATGAAGCAGCAGCTTCTTCAAGTCGCGC 264
QY 220 ATGAAGAAGCTTTGACAGGTCTATCCCAAGCGCTTCCAGTGGGCAAACTTACA 277
DB 265 ATGCCGGAAGGTAGCTCCAGGAGCGCACCATCTTCTTCAAGGACGACGCGCACTACA 322

RESULT 11
US-11-170-693-70
Sequence 70, Application US/11170693
Publication No. US20060014186A1
GENERAL INFORMATION:
APPLICANT: Hodges, Timothy A.
TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN
FILE REFERENCE: 023131.41500
CURRENT APPLICATION NUMBER: US/11/170,693
CURRENT FILING DATE: 2005-06-29
PRIOR APPLICATION NUMBER: 60/230,371
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 09/945,952
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 11/074,995
PRIOR FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: 11/
PRIOR FILING DATE: 2005-06-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.2
SEQ ID NO 70
LENGTH: 725
TYPE: DNA
ORGANISM: Mus sp.
US-11-170-693-70

Query Match 13.1%; Score 38; DB 12; Length 725;
Best Local Similarity 57.6%; Pred. No. 0.46;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAGAGCGCCAAAGCGCTCACCGGCCCAATGAATTCCTTCCAAAGGCGCGC 219

Db 208 GTGCAGTGTTCAGCGCTACCCGACCATGAGCAGCAGGACTTCTTCAAGTCCGCC 267
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGACCGCTTCACGGTGGGCAAAACCTTACA 277
Db 268 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 325

RESULT 12

US-11-175-690-115
; Sequence 115, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseitine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 115
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-175-690-115

Query Match 13.1%; Score 38; DB 12; Length 726;
Best Local Similarity 57.6%; Pred. No. 0.46;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAAGAGCGCAAGCGCTACCGGCCCAATGAATTCCTTCCGCTTCTTCAAGGCGGC 219
Db 211 GTGCAGTGTTCAGCGCTACCCGACCATGAGCAGCAGGACTTCTTCAAGTCCGCC 270
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGACCGCTTCACGGTGGGCAAAACCTTACA 277
Db 271 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 328

RESULT 13

US-11-069-642-46
; Sequence 46, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 46
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Synechocystis PCC6803
US-11-069-642-46

Query Match 13.1%; Score 38; DB 12; Length 1314;
Best Local Similarity 57.6%; Pred. No. 0.48;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAAGAGCGCAAGCGCTACCGGCCCAATGAATTCCTTCCGCTTCTTCAAGGCGGC 219
Db 610 GTGCAGTGTTCAGCGCTACCCGACCATGAGCAGCAGGACTTCTTCAAGTCCGCC 669
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGACCGCTTCACGGTGGGCAAAACCTTACA 277
Db 670 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 727

RESULT 14

US-11-069-642-48
; Sequence 48, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 48
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Synechocystis PCC6803
US-11-069-642-48

Query Match 13.1%; Score 38; DB 12; Length 1314;
Best Local Similarity 57.6%; Pred. No. 0.48;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAAGAGCGCAAGCGCTACCGGCCCAATGAATTCCTTCCGCTTCTTCAAGGCGGC 219
Db 610 GTGCAGTGTTCAGCGCTACCCGACCATGAGCAGCAGGACTTCTTCAAGTCCGCC 669
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGACCGCTTCACGGTGGGCAAAACCTTACA 277
Db 670 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 727

RESULT 15

US-11-069-642-50
; Sequence 50, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:

```

; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 03/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Synecchocystis PCC6803
US-11-069-642-50

```

Query Match	13.1%;	Score 38;	DB 12;	Length 1314;
Best Local Similarity	57.6%;	Pred. No. 0.48;	Indels 0;	Gaps 0;
Matches	68;	Conservative	0;	Mismatches 50;

QY	160	GTGAAGAGCGCCAAAGCGGCTTCACGGGCCCAATGAACTTCGCTTCCTCTCAAGGGCGGC	219
Db	610	GTTCAGTGTCTTACGCGCTACCCCGACCATGAAGCAGACGACGACTTCTTCAAGTCGCGCC	669
QY	220	ATGAAGAACTCTTTTCAGACGAGGTCATCCCCACCGCCTTCACGGTCGGCAAAACCTACA	277
Db	670	ATSCCGAAGGCTACGTCACGAGCGCACCATCTTCTTCAAGACGACGGCAACTACA	727

Search completed: February 17, 2006, 19:19:32
Job time : 300 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 18:13:13 ; Search time 806 Seconds
(without alignments)
2985.594 Million cell updates/sec

Title: US-10-628-296A-1
Perfect score: 291
Sequence: 1 acaaaagtcgatttaactgt.....octacacccagaatacaat 291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	100.0	291	7	US-10-628-296A-1
2	289.4	99.5	291	7	US-10-628-296A-3
3	91.4	31.4	1123	8	US-10-425-115-85501
4	91	31.3	1072	8	US-10-425-115-85503
5	89.8	30.9	1091	8	US-10-425-115-85499
6	89	30.6	1291	8	US-10-425-115-13007
7	86.6	29.8	1040	8	US-10-425-115-85498
8	84.2	28.9	1223	8	US-10-425-115-13012
9	84.2	28.9	1294	8	US-10-425-115-13005
10	82.6	28.4	1097	7	US-10-425-114-13857
11	82.6	28.4	1169	8	US-10-425-115-13010
12	82.6	28.4	1321	8	US-10-425-115-13967
13	82.2	28.2	720	3	US-09-949-888-1
14	80	27.5	681	7	US-10-437-963-95391
15	80	27.5	1292	7	US-10-437-963-95394
16	79.2	27.2	1253	7	US-10-425-114-26113
17	79.2	27.2	1253	8	US-10-425-115-5960
18	79.2	27.2	1289	7	US-10-767-701-15797
19	72	24.7	1252	7	US-10-767-701-15792
20	72	24.7	1283	7	US-10-767-701-15803
21	70.4	24.2	763	7	US-10-767-701-15780
22	69.8	24.0	1133	7	US-10-767-701-12975
23	68.6	23.6	306	3	US-09-294-093B-4181

24	67.2	23.1	928	7	US-10-437-963-95392	Sequence 95392, A
25	66.8	23.0	807	7	US-10-260-238-5775	Sequence 5775, Ap
26	66.8	23.0	1029	7	US-10-425-114-14004	Sequence 14004, A
27	66.8	23.0	1047	7	US-10-425-114-28997	Sequence 28997, A
28	66.8	23.0	1062	7	US-10-425-114-12890	Sequence 12890, A
29	66.8	23.0	1131	8	US-10-425-115-72506	Sequence 72506, A
30	66.8	23.0	1337	8	US-10-425-115-72520	Sequence 72520, A
31	66.8	23.0	1346	8	US-10-425-115-72510	Sequence 72510, A
32	66.2	22.7	1110	7	US-10-437-963-80639	Sequence 80639, A
33	65.2	22.4	1174	8	US-10-425-115-72518	Sequence 72518, A
34	65	22.3	609	7	US-10-425-114-3876	Sequence 3876, Ap
35	65	22.3	1273	5	US-10-125-001-3	Sequence 3, Appli
36	65	22.3	1273	10	US-11-142-525-3	Sequence 3, Appli
37	63.6	21.9	547	7	US-10-767-701-20877	Sequence 20877, A
38	62	21.3	969	7	US-10-425-114-17715	Sequence 17715, A
39	61.2	21.0	330	7	US-10-260-238-720	Sequence 720, App
40	61.2	21.0	647	7	US-10-767-701-15791	Sequence 15791, A
41	61.2	21.0	801	7	US-10-437-963-49284	Sequence 49284, A
42	60.4	20.8	405	8	US-10-425-115-165598	Sequence 165598, A
43	60.4	20.8	611	8	US-10-425-115-72505	Sequence 72505, A
44	60.4	20.8	1089	7	US-10-425-114-17864	Sequence 17864, A
45	60.4	20.8	3229	8	US-10-425-115-72516	Sequence 72516, A

ALIGNMENTS

RESULT 1
US-10-628-296A-1
; Sequence 1, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Lolium perenne
US-10-628-296A-1

Query Match	100.0%	Score 291;	DB 7;	Length 291;
Best Local Similarity	100.0%	Pred. No. 3.3e-75;		
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACAAAGTCGATTAACTGTGCGAAGGGTCTTGCAGGAGACGCTGGTGTGTAACATC	60	
Db	1	ACAAAGTCGATTAACTGTGCGAAGGGTCTTGCAGGAGACGCTGGTGTGTAACATC	60	
QY	61	AAGTACACGAGCGGCGGAGCACCTGCGGAGGTGGAGCTCCGCGACGACGCGCTCGGAG	120	
Db	61	AAGTACACGAGCGGCGGAGCACCTGCGGAGGTGGAGCTCCGCGAGCGGCTCGGAG	120	
QY	121	GAGTGGGAACCATGACCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTC	180	
Db	121	GAGTGGGAACCATGACCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTC	180	
QY	181	ACCGGCCCAATGAATTCGGCTTCTCTCCAAAGGCGGCATGAAGACGCTTTCGACGAG	240	
Db	181	ACCGGCCCAATGAATTCGGCTTCTCTCCAAAGGCGGCATGAAGACGCTTTCGACGAG	240	
QY	241	GTCAATCCCGCGCTTCACCGTGGGCAAAACCTTACCCCGCAATCAAT	291	
Db	241	GTCAATCCCGCGCTTCACCGTGGGCAAAACCTTACCCCGCAATCAAT	291	

RESULT 2

US-10-628-296A-3
; Sequence 3, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Lolium perenne
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Conservatively modified variant; C=substituted nucleotide

US-10-628-296A-3

Query Match 99.5%; Score 289.4; DB 7; Length 291;
Best Local Similarity 99.7%; Pred. No. 9.8e-75;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGGAGACGCTGGTGTGAACATC 60
DB 1 ACAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGGAGACGCTGGTGTGAACATC 60
QY 61 AAGTACACGAGCCAGGAGGACACCTTGGCGGAGGTGGAGTCCGGCAGCAGCGCTCGGAG 120
DB 61 AAGTACACGAGCCAGGAGGACACCTTGGCGGAGGTGGAGTCCGGCAGCAGCGCTCGGAG 120
QY 121 GAGTGGGAACCCATGACGAGAGGGGACACCTGTGGGAGGTGAAGAGCGCCAAAGCGCTC 180
DB 121 GAGTGGGAACCCCTGACGAGAGGGGACACCTGTGGGAGGTGAAGAGCGCCAAAGCGCTC 180
QY 181 ACCGGCCCAATGAATTCGGCTTCTCTCCAGGGGGCGCATGAAGAGCTTCGACGAG 240
DB 181 ACCGGCCCAATGAATTCGGCTTCTCTCCAGGGGGCGCATGAAGAGCTTCGACGAG 240
QY 241 GTCATCCCCCAGCGCTTACGGTCCGCAAAACCTACACCCCAAGATACAAT 291
DB 241 GTCATCCCCCAGCGCTTACGGTCCGCAAAACCTACACCCCAAGATACAAT 291

RESULT 3

US-10-425-115-85501
; Sequence 85501, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85501
; LENGTH: 1123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177986C.1

US-10-425-115-85501

Query Match 31.4%; Score 91.4; DB 8; Length 1123;
Best Local Similarity 59.4%; Pred. No. 1.2e-16;
Matches 174; Conservative 0; Mismatches 116; Indels 3; Gaps 1;
QY 2 CAAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGGAGACGCTGGTGTGAACATCA 61
DB 602 CTAAGGTCACTTCCACTTGGAGAGGGGTGCAACCCCACTACTCTGGCCCTGTGGTCA 661
QY 62 AGTACACGAGCCAGGGGACACCTTGGCGGAGGTGGAGTCCGGCAGCAGCGCTCGGAGG 121
DB 662 AGTACGTGAGCGGCGATGGCGACATTTGTGGCGGTGGACATCAAGGAGAGGGCTCCGACA 721
QY 122 AGTGGGAACCCATGACCAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCCAAGCGC 178
DB 722 CGTACGAGCCTCTAAAGCATCTCTGGGGCGCCATCTGGAGGAAGACACGACCAAGCGCA 781
QY 179 TCACGGGCCCAATGAATTCGGCTTCTCTCCAGGGGGCGCATGAAGAACGTTCTTCGACG 238
DB 782 TCAAGGAGCCATCACCGTCCAACTCACACCGAGGAGGCACCTAAGACCGTCTATGACG 841
QY 239 AGGTCAATCCCAACCGCCTTACGGTCCGCAAAACCTACACCCCAAGATACAAT 291
DB 842 ATGTATATCCCGCGGCTGGAAAGCCCAACACTGCTGTACACCGCCAAATAAACT 894

RESULT 4

US-10-425-115-85503
; Sequence 85503, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85503
; LENGTH: 1072
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177988C.1

US-10-425-115-85503

Query Match 31.3%; Score 91; DB 8; Length 1072;
Best Local Similarity 59.5%; Pred. No. 1.5e-16;
Matches 173; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
QY 2 CAAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGGAGACGCTGGTGTGAACATCA 61
DB 585 CTAAGGTCACTTCCACTTGGAGAGGGGTGCAACCCCACTACTCTGGCCCTGTGGTCA 644
QY 62 AGTACACGAGCCAGGGGACACCTTGGCGGAGGTGGAGTCCGGCAGCAGCGCTCGGAGG 121
DB 645 AGTACGTGTATGGAGATGCTGACATTTGTGGCGGTGGACATCAAGGAGAGGGCTCTGACA 704
QY 122 AGTGGGAACCCATGACCAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCCAAGCGCG 178
DB 705 CTAAGGCTCTTGAAGCATCTTGGGGCGCCATCTGGAGGAGATAGGACCAAGCGCA 764
QY 179 TCACCGGGCCCAATGAATTCGGCTTCTCTCCAGGGGGCGCATGAAGAACGTTCTTCGACG 238
DB 765 TCAAGGAGCCCATCACCGTCCGACTCACACCGAGGGAGGCACCTAAGACTGTCTACGAG 824
QY 239 AGGTCAATCCCAACCGCCTTACGGTCCGCAAAACCTACACCCCAAGATACA 289
DB 825 ACGTATATCCCGCGGCTGGAAAGCCCAACACTGCTGTACACCCCAATGATAGA 875

RESULT 5
US-10-425-115-85499
; Sequence 85499, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85499
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177984C.1
US-10-425-115-85499

Query Match 30.9%; Score 89.8; DB 8; Length 1091;
Best Local Similarity 59.0%; Pred. No. 3.4e-16;
Matches 173; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 2 CAAAGTTCGATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTGAACATCA 61
DB 584 CTAAGGTCACTTCCACTTGGAGAGGGGTGCAACCCCAACTACCTGGCACTGTGGTCA 643

QY 62 AGTACACGAGCCAGGGGACACCCCTGGCGGAGGTGGAGTCCGGCAGCACGCTCGGAGG 121
DB 644 AGTACGTCAGCGCATGGCGACATTTGGCGGTGGACATCAAGAGAAGGGCTCCGACA 703

QY 122 AGTGGGAACCCATGATCAGGAAGAA--GGGCAACCTGTGGGAGGTGAAGAGCGCGCAAGCGC 178
DB 704 CGTACGAGCCCTAAAGCACTCTCTGGGCGGCATCTGGAGGAAGACAGACGACGCGA 763

QY 179 TCACCGGCGCCATGNACTTCGCTTCCTCTCAAGGGCGGCATGAAGAACGCTTTCGAGC 238
DB 764 TCAAGGGAGCCCATCACTCCGCTCCAACTCACCACCGAGGAGGCACCTAAGACCGCTATGACG 823

QY 239 AGGTCACTCCCAACCGCTTTCAGGTCGCGCAAAACCTACACCCCAAGATACAT 291
DB 824 ATGTATCCCGCTGGCTGGAAGCCCAACACTGCTACACCGCCAAATAACT 876

RESULT 6
US-10-425-115-13007
; Sequence 13007, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13007
; LENGTH: 1291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111859C.1
US-10-425-115-13007

Query Match 30.6%; Score 89; DB 8; Length 1291;
Best Local Similarity 59.2%; Pred. No. 5.9e-16;
Matches 171; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 2 CAAAGTTCGATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTGAACATCA 61
DB 566 CCAAGGTCACTTCCATCTTGAAAGAGGGGTGGGCCCCCAACTACCTGGCGCTGTGGTCA 625

QY 62 AGTACACGAGCCAGGGGACACCCCTGGCGGAGGTGGAGTCCGGCAGCACGCTCGGAGG 121
DB 626 AGTACGTCAGCGCGACGGTGACATTTGGCGGTGGACATCAAGAGAAGGGCTCCGACA 685

QY 122 AGTGGGAACCCATGATCAGGAAGAA--GGGCAACCTGTGGGAGGTGAAGAGCGCAAGCGCGC 178
DB 686 CGTACGAGCCCTGAAGCACTCTTGGCGTGCCTCTCGAGGAAGGACAGCGCAAAACCGC 745

QY 179 TCACCGGCGCCATGNACTTCGCTTCCTCTCAAGGGCGGCATGAAGAACGCTTTCGAGC 238
DB 746 TTAAGGGAGCCCTCACCGTCCGCTCACTACCGAGGAGGCACCAAGACCGCTTACGAGC 805

QY 239 AGGTCACTCCCAACCGCTTTCAGGTCGCGCAAAACCTACACCCCAAGATA 287
DB 806 ATGTATCCCTGCCCACTTGGAGGCCAACACCGCTTACACCGCCAAATA 854

RESULT 7
US-10-425-115-85498
; Sequence 85498, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85498
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177983C.1
US-10-425-115-85498

Query Match 29.8%; Score 86.6; DB 8; Length 1040;
Best Local Similarity 58.4%; Pred. No. 2.9e-15;
Matches 171; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAAGTTCGATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTGAACATCA 61
DB 563 CTAAGGTCACTTCCATTTGGAGAGGGATGCAACCCCAACTACCTGGCGCTGTGGTAA 622

QY 62 AGTACACGAGCCAGGGGACACCCCTGGCGGAGGTGGAGTCCGGCAGCACGCTCGGAGG 121
DB 623 AGTACGTTGTGGAGATGGTGACATTTGGCAGTGGACATTAAGAGAAGGGCTCTGACA 682

QY 122 AGTGGGAACCCATGACGAAGAA--GGGCAACCTGTGGGAGGTGAAGAGCGCGCAAGCGCGC 178
DB 683 CGTACGAGCCCTTAAGACACTCTCTGGGTGGTCCATCTGGAGGAAGACAGACGACGACAA 742

QY 179 TCACCGGCGCCATGAACTTCGCTTCCTCTCAAGGGCGGCATGAAGAACGCTTTCGAGC 238
DB 743 TCAAGGGAGCCCATCACCGTCCGACTCACCAACCGAGGAGGCACCTAAGACTGTCTACGAGC 802

QY 239 AGGTCACTCCCAACCGCTTTCAGGTCGCGCAAAACCTACACCCCAAGATACAT 291
DB 803 ACGTCATACCCACCGACTGGGAAGCCCAACACCGCTTACACCCCAATAAACT 855

RESULT 8
US-10-425-115-13012
; Sequence 13012, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13012
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111863C.1
US-10-425-115-13012

Query Match 28.9%; Score 84.2; DB 8; Length 1223;
Best Local Similarity 58.1%; Pred. No. 1.5e-14;
Matches 168; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTTAACTGTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGTAACATCA 61
DB 597 CCAAGGTCACCTTCCACCTTGAAAGGGGTGGGGCCCACTACCTGGCACTGTGGTCA 656
QY 62 AGTACACAGGCGGAGGACACCCCTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGG 121
DB 657 AGTACGTCGACGGGACGCGGTGACATTTGGGAGTGGAGCTCAAGGAGAGGGGCTCCGACA 716
QY 122 AGTGGGAACCCATGACGAGA---AGGGCAACCTGTGGAGGTGAAGAGCGCGCAAGCGCG 178
DB 717 CGTACGAGCCCTGAAGCACTCTCTGGGGGCCATCTGGAGGAGGACAGCGACAAACCGC 776
QY 179 TCACCGGCGCCAAATGAACCTTCGGCTTCCTCCAGGGCGGCGATGAAGAACGCTTTCGAGC 238
DB 777 TTAAGGAGCCCTCACCCTGCGGCTCACTACCGAGGGAGGACCAAGTCCGCTCTACGAGC 836
QY 239 AGGTCATCCCGACCGCTTCAGGTCGGCGGCAAACTACACCCCAAGATA 287
DB 837 ATGTCATCCCTGCCAACTGGAAGGCCAACACCGCCTACACCGCCAAATA 885

RESULT 9
US-10-425-115-13005
; Sequence 13005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13005
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111857C.1
US-10-425-115-13005

Query Match 28.9%; Score 84.2; DB 8; Length 1294;
Best Local Similarity 58.1%; Pred. No. 1.5e-14;

Matches 168; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTTAACTGTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGTAACATCA 61
DB 600 CCAAGGTCACCTTCCACCTTGAAAGGGGTGGGGCCCACTACCTGGCGTGGTGTAGTCA 659
QY 62 AGTACACAGGCGGAGGACACCCCTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGG 121
DB 660 AGTACGTCGACGGGCGGCGGTGACATTTGGCGGTGGAGCTCAAGGAAAGGGCTCCGACA 719
QY 122 AGTGGGAACCCATGACGAGA---AGGGCAACCTGTGGAGGTGAAGAGCGCGCAAGCGCG 178
DB 720 CGTACGAGCCCTCAAGCACTCTCTGGGGCGCCATCTGGAGGAGGACAGCGACAAACCGC 779
QY 179 TCACCGGCGCCAAATGAACCTTCGGCTTCCTCCAGGGCGGCGATGAAGAACGCTTTCGAGC 238
DB 780 TTAAGGAGCCCTCACCCTGCGCTCACTACCGAGGAGGACCAAGACCGCTCTACGAGC 839
QY 239 AGGTCATCCCGACCGCTTCACGTCGGCGGCAAACTACACCCCAAGATA 287
DB 840 ATGTCATCCCTGCCAACTGGAAGGCCAACACCGCCTACACCGCCAAATA 888

RESULT 10
US-10-425-114-13857
; Sequence 13857, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13857
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-004-A3_FLI
US-10-425-114-13857

Query Match 28.4%; Score 82.6; DB 7; Length 1097;
Best Local Similarity 57.8%; Pred. No. 4.3e-14;
Matches 167; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTTAACTGTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGTAACATCA 61
DB 543 CCAAGGTCACCTTCCACCTTGAAAGGGGTGGCGCCCACTACCTGGCACTGTGGTCA 602
QY 62 AGTACACAGGCGGAGGAGACACCCCTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGG 121
DB 603 AGTACGTCGACGGGCGGCGGTGACATTTGGCAGTGGAGCTCAAGGAGAGGGGCTCCGACA 662
QY 122 AGTGGGAACCCATGACGAGA---AGGGCAACCTGTGGAGGTGAAGAGCGCGCAAGCGCG 178
DB 663 CGTACGAGCCTCTGAAGCACTCTCTGGGGCGCCATCTGGAGGAGGACAGCGACAAACCGC 722
QY 179 TCACCGGCGCCAAATGAACCTTCGGCTTCCTCCAGGGCGGCGATGAAGAACGCTTTCGAGC 238
DB 723 TTAAGGAGCCCTCACCCTGCGCTCACTACCGAGGAGGACCAAGTCCGCTCTACGAGC 782
QY 239 AGGTCATCCCGACCGCTTCACGTCGGCGGCAAACTACACCCCAAGATA 287
DB 783 ATGTCATCCCTGCCAACTGGAAGGCCAACACCGCCTACACCGCCAAATA 831

RESULT 11
US-10-425-115-13010
; Sequence 13010, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13010
; LENGTH: 1169
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_111861C.1
US-10-425-115-13010

Query Match 28.4%; Score 82.6; DB 8; Length 1169;
Best Local Similarity 57.8%; Pred. No. 4.4e-14;
Matches 167; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTAACTGTGGAGAGGGTCTTACGCGAAGACGCTGGTGTCTGAACATCA 61
DB 596 CCAAGTCACTTCCACCTTGAAGAGGGTGGCGGCCCACTACTTGGCACTGTGGTCA 655

QY 62 AGTACACAGGCGCAGGGACACCCCTGGCGGAGGTGGAGCTCGGCAGCACCGCTCGGAGG 121
DB 656 AGTACGTGCGCGCGACGGTGCATTTGTGGCAGTGGACCTCAAGGAGAAGGGCTCCGACA 715

QY 122 AGTGGARACCATGACGAGA---AGGGCAACCTGTGGAGGTGAAGAGCGCCAGCGCG 178
DB 716 CGTAGCGACCTCTGAAGCACTCTCTGGGGCGCCATCTGGAGGAAGGACAGCGCAACCGC 775

QY 179 TCACCGGCCCAATGAATTCGCTTCTTCCAAAGGGCGGATGAAGAACGCTTTCGACG 238
DB 776 TTAGGGACCCCTACCGCTCGCCTCACTACGAGGAGGACCAAGTCCGCTTACGACG 835

QY 239 AGGTCAATCCCAACCGCTTCAAGTTCGCGCAAAACCTACACCCCAATA 287
DB 836 ATGTCAATCCCTGCCAACTTGAAGGCAACACCGCTTACACCGCCAAATA 884

RESULT 12
US-10-425-115-39657
; Sequence 39657, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 39657
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_136168C.1
US-10-425-115-39657

Query Match 28.4%; Score 82.6; DB 8; Length 1321;
Best Local Similarity 57.8%; Pred. No. 4.5e-14;

Matches 167; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTAACTGTGGAGAGGGTCTTACGCGAAGACGCTGGTGTCTGAACATCA 61
DB 595 CCAAGTCACTTCCACCTTGAAGAGGGTGGCGGCCCACTACTTGGCACTGTGGTCA 654

QY 62 AGTACACAGGCGCAGGGACACCCCTGGCGGAGGTGGAGCTCGGCAGCACCGCTCGGAGG 121
DB 655 AGTACGTGCGCGCGACGGTGCATTTGTGGCAGTGGACGCTCAAGGAGAAGGGCTCCGACA 714

QY 122 AGTGGARACCATGACGAGA---AGGGCAACCTGTGGAGGTGAAGAGCGCCAGCGCG 178
DB 715 CATACGAGCCCTGAAGCACTCTCTGGGGCGCCATCTGGAGGAAGGACAGCGCAACCGC 774

QY 179 TCACCGGCCCAATGAATTCGCTTCTTCCAAAGGGCGGATGAAGAACGCTTTCGACG 238
DB 775 TTAGGGACCCCTCAACCGCTCGCCTCACTACGAGGAGGACCAAGTCCGCTTACGACG 834

QY 239 AGGTCAATCCCAACCGCTTCAAGTTCGCGCAAAACCTACACCCCAATA 287
DB 835 ATGTCAATCCCTGCCAACTTGAAGGCAACACCGCTTACACCGCCAAATA 883

RESULT 13
US-09-949-888-1
; Sequence 1, Application US/09949888
; Patent No. US20020064530A1
; GENERAL INFORMATION:
; APPLICANT: CONSIGLIO NAZIONALE DELLE RICERCHE
; TITLE OF INVENTION: VARIANTS OF PHEUM PRATENSE ALLERGENIC PROTEINS
; FILE REFERENCE: CNR
; CURRENT APPLICATION NUMBER: US/09/949,888
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Pheum pratense
US-09-949-888-1

Query Match 28.2%; Score 82.2; DB 3; Length 720;
Best Local Similarity 58.4%; Pred. No. 5.3e-14;
Matches 163; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

QY 1 ACAAAGTCGATTAACTGTGGAGAGGGTCTTCAAGCGAAGACGCTGGTGTCTGAACATC 60
DB 433 ACCAAGGTGACCTTCCAGCTGGAGAGGGTCTCAACCCCACTACCTGGCGCTGCTGTG 492

QY 61 AAGTACACGAGGCGCAGGGGACACCCCTGGCGAGGTGGAGCTTCGGCAGACGCGCTCGGAG 120
DB 493 AAGTACGTTAAACGCGCAGGAGACGCTGGTGGCGTGGACATCGCGAGGCGGCGGAC 552

QY 121 GAGTGG---GAAACCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGG 177
DB 553 GCGTGGATCGAGCTCAAGAGAGTCTGGGGAGCCATCTGGAGGATCGACACTCCCGACAAG 612

QY 178 CTCACCGGCCCAATGAATTCGCTTCTTCCAAAGGGCGGCGCATGAAGACGCTTCTCGAC 237
DB 613 CTCACGGGCCCCCTTACCGCTTACACCAACCGAGGCGGCACCAAGACCGAAGCCGAG 672

QY 238 GAGGTCAATCCCAACCGCTTCCAGCTGGCGGCAAAACCTTAC 276
DB 673 GACGTCAATCCCTGAGGGCTGGAAGCGCGACACCAAGTAC 711

RESULT 14
US-10-437-963-95391
; Sequence 95391, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 95391
LENGTH: 681
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_93590C.1
US-10-437-963-95391

Query Match 27.5%; Score 80; DB 7; Length 681;
Best Local Similarity 57.9%; Pred. No. 2.3e-13;
Matches 162; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
Qy 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGGTGAACATC 60
Db 379 ACCAAGATCACCTTCCACATCGAGAAGGCCCTCCAAACCCCAACTACCTTGGCGTGTAGTC 438
Qy 61 AAGTACACGAGGCGCAGGGGACACCTGGCGGAGGTGGAGCTCCGCGCAGCAGCGGCTCGGAG 120
Db 439 AAGTACGTCGCTGGTGATGGTGACGCTGTGGAGGTGGAATCAAGGAGAGGGCTCCGAG 498
Qy 121 GAGTGGGAACCCATGACGAAGAA---GGGCACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 499 GAGTGGGAAGGCGCTCAAGGAGTCATGGGGTGCATTGAGAGGATAGACACCCCAAGCCG 558
Qy 178 CTCACCGGCCCAATGAATTCGCTTCTCCAGGGCGGCATGAAGACGCTTCGAC 237
Db 559 CTCAGGGGCCCTTCTCCGTCGCGTCACCCAGAGGTGGCGAGAGATCATGCCCGAG 618
Qy 238 GAGGTATCCCGCCACCGCCTTACGGTCGCGCAAAACCTACA 277
Db 619 GACGCCATCCCTGATGGCTGGNAGGCCGACAGCGGTGTACA 658

RESULT 15
US-10-437-963-95394
Sequence 95394, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 95394
LENGTH: 1292
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_93593C.1
US-10-437-963-95394

Query Match 27.5%; Score 80; DB 7; Length 1292;

Best Local Similarity 57.9%; Pred. No. 2.6e-13;
Matches 162; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
Qy 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGGTGAACATC 60
Db 557 ACCAAGATCACCTTCCACATCGAGAAGGCCCTCCAAACCCCAACTACCTTGGCGTGTAGTC 616
Qy 61 AAGTACACGAGGCGCAGGGGACACCTGGCGGAGGTGGAGCTCCGCGCAGCAGCGGCTCGGAG 120
Db 617 AAGTACGTCGCTGGTGATGGTGACGCTGTGGAGGTGGAATCAAGGAGAGGGCTCCGAG 676
Qy 121 GAGTGGGAACCCATGACGAAGAA---GGGCACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 677 GAGTGGGAAGGCGCTCAAGGAGTCATGGGGTGCATTGAGAGGATAGACACCCCAAGCCG 736
Qy 178 CTCACCGGCCCAATGAATTCGCTTCTCCAGGGCGGCATGAAGACGCTTCGAC 237
Db 737 CTCAGGGGCCCTTCTCCGTCGCGTCACCCAGAGGTGGCGAGAGATCATGCCCGAG 796
Qy 238 GAGGTATCCCGCCACCGCCTTACGGTCGCGCAAAACCTACA 277
Db 797 GACGCCATCCCTGATGGCTGGNAGGCCGACAGCGGTGTACA 836

Search completed: February 17, 2006, 21:07:44
Job time : 808 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 18:08:44 ; Search time 145 Seconds
(without alignments)

3567.382 Million cell updates/sec

Title: US-10-628-296A-1

Perfect score: 291

Sequence: 1 acaaaagtcgatttaactgt.....cctacacccagaatacaat 291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79.2	27.2	1072	2	US-07-971-096-1
2	79.2	27.2	1072	2	US-08-175-096-1
3	77.6	26.7	802	3	US-08-441-507-18
4	77.6	26.7	802	3	US-07-969-875A-18
5	76	26.1	759	3	US-08-441-507-20
6	76	26.1	759	3	US-07-969-875A-20
7	76	26.1	775	3	US-08-441-507-3
8	76	26.1	775	3	US-07-969-875A-3
9	76	26.1	832	3	US-08-441-507-19
10	76	26.1	832	3	US-07-969-875A-19
11	71	24.4	756	3	US-08-413-974-3
12	71	24.4	756	3	US-08-434-418-3
13	71	24.4	756	3	US-08-433-288-3
14	71	24.4	756	3	US-08-174-739A-3
15	71	24.4	756	3	US-08-434-256-3
16	69.4	23.8	810	3	US-08-413-974-5
17	69.4	23.8	810	3	US-08-434-418-5
18	69.4	23.8	810	3	US-08-433-288-5
19	69.4	23.8	810	3	US-08-174-739A-5
20	69.4	23.8	810	3	US-08-434-256-5
21	69.4	23.8	1123	2	US-07-971-096-3
22	69.4	23.8	1123	2	US-08-175-096-3
23	68.8	23.6	662	3	US-08-441-507-1
24	68.8	23.6	662	3	US-07-969-875A-1

Sequence 17, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 9106, Ap
Sequence 973, App
Sequence 23, Appl
Sequence 21, Appl
Sequence 56, Appl
Sequence 53, Appl
Sequence 5079, Ap
Sequence 1036, Ap
Sequence 6280, Ap
Sequence 371, App
Sequence 5, Appl
Sequence 13416, A
Sequence 13732, A
Sequence 16168, A
Sequence 16059, A
Sequence 16424, A

25 67.2 23.1 594 3 US-08-441-507-17
26 67.2 23.1 594 3 US-07-969-875A-17
27 54.4 18.7 1378 3 US-09-071-252-4
28 46.6 16.0 1776 3 US-09-679-686B-11
29 45.6 15.7 623 3 US-09-902-540-9106
30 45.6 15.7 10318 3 US-09-902-540-973
31 45.4 15.6 2664 3 US-10-132-350-23
32 45.4 15.6 2664 3 US-10-132-350-27
33 45.4 15.6 3122 3 US-10-132-350-21
34 45.4 15.6 4483 3 US-10-132-350-56
35 45.4 15.6 7492 3 US-10-132-350-53
36 45.2 15.5 2975 3 US-09-902-540-5079
37 45.2 15.5 12950 3 US-09-902-540-1036
38 42.8 14.7 525 3 US-09-902-540-6280
39 42.8 14.7 1644 3 US-09-902-540-371
40 42.4 14.6 1392 3 US-09-071-252-5
41 42 14.4 1629 3 US-09-252-991A-13416
42 42 14.4 1731 3 US-09-252-991A-13732
43 41.6 14.3 1485 3 US-09-252-991A-16168
44 41.6 14.3 1548 3 US-09-252-991A-16059
45 41.6 14.3 1587 3 US-09-252-991A-16424

ALIGNMENTS

RESULT 1

US-07-971-096-1
; Sequence 1, Application US/07971096
; Patent No. 5480972
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Avjoglu, Asil
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: ALLERGENIC PROTEINS AND PEPTIDES FROM
; TITLE OF INVENTION: JOHNSON GRASS POLLEN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,096
; FILING DATE: 19921030
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-042 (IMI-022)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1072 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 37..822
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 109..822
US-07-971-096-1

Query Match 27.2%; Score 79.2; DB 2; Length 1072;
Best Local Similarity 56.8%; Pred. No. 3.1e-09;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 3 AAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGTGCTGGAACATCAA 62
Db 537 AAAGTCACCTTCCACGTGGAGAGGGGAGCAACCCCAACTACCTGTGTTGGTCAA 596
QY 63 GTACACGAGGCCAGGGACACCTTGGCGGAGGTGAGCTCCGCGACGACGCTCGGAGGA 122
Db 597 GTACGTGCAGCGGACGCTGACGTTGTGGGGGTGGAATCAAGAGAGGGGTGGCGACG 656
QY 123 GTGGGAACCCATGACGAGAA---GGCAACCTGTGGAGGTGAAGAGCGCCAGCGCT 179
Db 717 CAAAGTTTCCCGTCAACGCTCAAAATCACCCGAGGAGGACCAAGACCGGCTACGAAGA 776
QY 240 GGTATCCCCACCGCTTCAGGTCGGCAAAACCTACACCCCAAGATCAAT 291
Db 777 CGTCATCCCCGAGGCTGGAAGGCCGACACCACTACACCGCCAAATAACT 828

RESULT 2
US-08-175-096-1
; Sequence 1, Application US/08175096
; Patent No. 5691167
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Avjoglu, Asil
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: ALLERGENIC PROTEINS AND PEPTIDES FROM
; TITLE OF INVENTION: JOHNSON GRASS POLLEN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175.096
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,096
; FILING DATE: OCT 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-042 (IMI-022)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1072 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..822
; NAME/KEY: mat_peptide
; LOCATION: 109..822
US-08-175-096-1

Query Match 27.2%; Score 79.2; DB 2; Length 1072;
Best Local Similarity 56.8%; Pred. No. 3.1e-09;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 3 AAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGTGCTGGAACATCAA 62
Db 537 AAAGTCACCTTCCACGTGGAGAGGGGAGCAACCCCAACTACCTGTGTTGGTCAA 596
QY 63 GTACACGAGGCCAGGGGACACCTTGGCGGAGGTGAGCTCCGCGACGACGCTCGGAGGA 122
Db 597 GTACGTGCAGCGGACGCTGACGTTGTGGGGGTGGAATCAAGAGAGGGGTGGCGACG 656
QY 123 GTGGGAACCCATGACGAGAA---GGCAACCTGTGGAGGTGAAGAGCGCCAGCGCT 179
Db 717 CAAAGTTTCCCGTCAACGCTCAAAATCACCCGAGGAGGACCAAGACCGGCTACGAAGA 776
QY 240 GGTATCCCCACCGCTTCAGGTCGGCAAAACCTACACCCCAAGATCAAT 291
Db 777 CGTCATCCCCGAGGCTGGAAGGCCGACACCACTACACCGCCAAATAACT 828

RESULT 3
US-08-441-507-18
; Sequence 18, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
```

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-441-507-18

Query Match 26.7%; Score 77.6; DB 3; Length 802;
Best Local Similarity 57.0%; Pred. No. 6.9e-09;
Matches 162; Conservative 0; Mismatches 119; Indels 3; Gaps 1;
QY 1 ACAAAGTCGATTAACTGTGAGAGAGGTTTCTGACGCGAAGACGCTGGTGTGTAACATC 60
DB 295 ACCAAGATCATCTCCACATCGAGAGGGATCCAAAGACCATATTACTTGGCGCTGCTCGTC 354
QY 61 AAGTACAGAGGCGGACACCTTGGCGAGGTGGAGCTCCGCGACACGCTCGGAG 120
DB 355 AAGTACGCGGCGGATGGCAACATTGTTGCTGCGACATCAAGCCCAAGGACTCCGAC 414
QY 121 GAGTGGGAACCATGACGAGAA--GGGCAACCTGTGGGAGGTGAAGAGCGCCAGCG 177
DB 415 GAGTTCATTCCCATGAAGTCGCTCTGGGGCGCCATCTGGAGGATCGACCCCAAGAGCG 474
QY 178 CTCACCGCCCAATGAATCTCCGCTTCTCCTCAAGGGCGGCATGAAGAGCTCTTCGAC 237
DB 475 CTCAGGGCCCTTCTCCATCCGCTCACCTCCGAGGGCGGGCCCATCTCGTCCAGAC 534
QY 238 GAGTTCATCCCAAGCGCTTCAAGTCCGCGGCAAAACCTACACCC 281
DB 535 GACGTATCCAGGCAACTGGAAGCCAGACACCGCTCTACACCTC 578

RESULT 4

US-07-969-875A-18
Sequence 18, Application US/07969875A
Patent No. 6441157
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species
TITLE OF INVENTION: Cynodon Dactylon
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation
STREET: 610 Lincoln Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,875A
FILING DATE: 30-October-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 041.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-969-875A-18

Query Match 26.7%; Score 77.6; DB 3; Length 802;
Best Local Similarity 57.0%; Pred. No. 6.9e-09;
Matches 162; Conservative 0; Mismatches 119; Indels 3; Gaps 1;
QY 1 ACAAAGTCGATTAACTGTGAGAGAGGTTTCTGACGCGAAGACGCTGGTGTGTAACATC 60
DB 295 ACCAAGATCATCTCCACATCGAGAGGGATCCAAAGACCATATTACTTGGCGCTGCTCGTC 354
QY 61 AAGTACAGAGGCGGACACCTTGGCGAGGTGGAGCTCCGCGACACGCTCGGAG 120
DB 355 AAGTACGCGGCGGATGGCAACATTGTTGCTGCGACATCAAGCCCAAGGACTCCGAC 414
QY 121 GAGTGGGAACCATGACGAGAA--GGGCAACCTGTGGGAGGTGAAGAGCGCCAGCG 177
DB 415 GAGTTCATTCCCATGAAGTCGCTCTGGGGCGCCATCTGGAGGATCGACCCCAAGAGCG 474
QY 178 CTCACCGCCCAATGAATCTCCGCTTCTCCTCAAGGGCGGCATGAAGAGCTCTTCGAC 237
DB 475 CTCAGGGCCCTTCTCCATCCGCTCACCTCCGAGGGCGGGCCCATCTCGTCCAGAC 534
QY 238 GAGTTCATCCCAAGCGCTTCAAGTCCGCGGCAAAACCTACACCC 281
DB 535 GACGTATCCAGGCAACTGGAAGCCAGACACCGCTCTACACCTC 578

RESULT 5

US-08-441-507-20
Sequence 20, Application US/08441507
Patent No. 6214358
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species Cynodon
TITLE OF INVENTION: Dactylon
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,507
FILING DATE: 15-May-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,875
FILING DATE: 30-October-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-049DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna

```

;
; NAME/KEY: CDS
; LOCATION: 1..738
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 742..759
US-08-441-507-20

```

Query Match	26.1%	Score 76	DB 3	Length 759
Best Local Similarity	56.7%	Pred. No. 1.6e-08		
Matches 161	Conservative 0	Mismatches 120	Indels 3	Gaps 1
Qy	1	ACAAAAGTCGATTTAACTGTGGGAAGAGGGTTCTACGCGAAGACGCTGGTCTCAACATC	60	
Db	436	ACCAAGATCACCTTCCACATCGAAGAGGATCCAACGACCATTAACCTGGCGCTCTCGTC	495	
Qy	61	AAGTACACGAGGCCAGGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCAGCGGTTCGGAG	120	
Db	496	AAGTACCGCGCGCGATGGCAACATTTGTGCGCGTCGCACATCAAGCCGAGGACTCCGAC	555	
Qy	121	GAGTGGGAACCCATGACGAAAGAA---GGGCAACCTGTGGGAGGTGAAGAGGCCCAAGCCG	177	
Db	556	GAGTTTCATTCCTCATGAAGTGTCTCTGGGGGCCATCTGGAGGATCGACCCCAAGAAGCCG	615	
Qy	178	CTCACGGGCCCAATGAATTCCTCGGCTTCTCTCAAGGGCGGCATGAAGAAGTCTTCGCAC	237	
Db	616	CTCAAGGGGCCCCCTTCTCATCGGCTCACCTTCGAGGGGCGGCCCATCTGCTCCAGGAC	675	
Qy	238	GAGGTCAATCCCAACCGCTTTCACGGTCGGCAAAACCTACACCC	281	
Db	676	GAGGTCAATCCCAACCACTGAAGCCAGACACCGTCTACACCTC	719	

RESULT 6

```

US-07-969-875A-20
; Sequence 20, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.,
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6090
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE:  cdna
; FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  1..738
; FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  742..759
US-07-969-875A-20

```

	Query Match	26.1%;	Score 76;	DB 3;	Length 759;
	Best Local Similarity	56.7%;	Pred. No. 1.6e-08;		
	Matches 161;	Conservative 0;	Mismatches 120;	Indels 3;	Gaps 1
Qy	1	ACAAAAGTCGATTTAACTGTGTGGAGAAAGGGTTCTGACGGAAGACGCTGTGCTGAACATC	60		
Db	436	ACCAAGATCACCTTCCACATCGAAGAGGGATCCAACGACCATTAACCTGGCGCTGCTGCTC	495		
Qy	61	AAGTACAGGAGCCAGGGGACACCTTCGGCGAGGTGGAGTCCGGGACGACGGTCCGAG	120		
Db	496	AAGTACGCGCGCGCGATGGCAATTTGTGCGCGTGCACATCAAGCCCAGGGACTCCCGAC	555		
Qy	121	GAGTGGGAACCCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGGCCCAAGCCG	177		
Db	556	GAGTTTCATTCCCATGAAGTCGTCTCTGGGCGCCATCTGGAGGATCGACCCCAAGAAGCG	615		
Qy	178	CTACCGGCGCAATGAATCTTCGGTTCTCTCCAAGGCGGCATGAAGAAAGTCTTCGAC	237		
Db	616	CTCAAGGGGCCCCCTTCTCATTCGGCTCACCTTCGAGGGGCGGCCCATCTCGTCAGGAC	675		
Qy	238	GAGGTCAATCCCCACCGCTTTCAGGTCGGCAAAACCTACACCCC	281		
Db	676	GAGTTCATCCAGCCAACTGGAGCCAGACACCGTCTACACCTC	719		

RESULT 7

RES001
 US-08-441-507-3
 ; Sequence 3, Application US/08441507
 ; Patent No. 6214358
 ; GENERAL INFORMATION:
 ; APPLICANT: Singh, Penelope; and
 ; APPLICANT: Knox, Robert Bruce
 ; APPLICANT: Mohan Bir;
 ; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
 ; TITLE OF INVENTION: Dactylon
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/441,507
 ; FILING DATE: 15-May-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/969,875
 ; FILING DATE: 30-October-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: IMI-049DV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 742-4214
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 775 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..600
US-08-441-507-3

Query Match 26.1%; Score 76; DB 3; Length 775;

Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1 ACAAAAGTCGATTAACTGTGTGAGAGGGTTCTGACGGCAAGACGCTGTGTGTGAACATC 60
DB ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAAGCAATTAATCTGGCGCTGTCTGTC 357
QY 61 AAGTACAGAGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGGAGCAGCAGCGCTCGGAG 120
DB AAGTACAGCGCGCGGGGATGGCAACATTTGTGCGCGTCGACATCAAGCCCAAGGACTCCGAC 417
QY 121 GAGTGGGAACCCATCAGCAAGAA---GGGCAACCTGTGGAGGTGAAGAGCCCAAGCG 177
DB GAGTTCAATTCCTTCCATGAGTGTCTTCCATCGCTTCCATCGAGGATCGACCCCAAGAGCG 477
QY 178 CTCACCGGCCCAATGAATTCCTTCCATCGCTTCCATCGAGGCGGCGATGAAGAACTCTTCGAC 237
DB CTCAGGGGCCCTTCTCCATCGCTTCCATCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 537
QY 238 GAGGTATCCCAACCGCTTACGCTCGGCAAAACCTACACCCC 281
DB GAGGTATCCCAACCGCTTACGCTCGGCAAAACCTACACCCC 581

RESULT 8

US-07-969-875A-3
Sequence 3, Application US/07969875A
Patent No. 6441157
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species
TITLE OF INVENTION: Cynodon Dactylon
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation
STREET: 610 Lincoln Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,875A
FILING DATE: 30-October-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A..
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 041.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..600
US-07-969-875A-3

Query Match 26.1%; Score 76; DB 3; Length 775;

Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1 ACAAAAGTCGATTAACTGTGTGAGAGGGTTCTGACGGCAAGACGCTGTGTGTGAACATC 60
DB ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAAGCAATTAATCTGGCGCTGTCTGTC 357
QY 61 AAGTACAGAGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGGAGCAGCAGCGCTCGGAG 120
DB AAGTACAGCGCGCGGGGATGGCAACATTTGTGCGCGTCGACATCAAGCCCAAGGACTCCGAC 417
QY 121 GAGTGGGAACCCATCAGCAAGAA---GGGCAACCTGTGGAGGTGAAGAGCCCAAGCG 177
DB GAGTTCAATTCCTTCCATGAGTGTCTTCCATCGCTTCCATCGAGGATCGACCCCAAGAGCG 477
QY 178 CTCACCGGCCCAATGAATTCCTTCCATCGCTTCCATCGAGGCGGCGATGAAGAACTCTTCGAC 237
DB CTCAGGGGCCCTTCTCCATCGCTTCCATCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 537
QY 238 GAGGTATCCCAACCGCTTACGCTCGGCAAAACCTACACCCC 281
DB GAGGTATCCCAACCGCTTACGCTCGGCAAAACCTACACCCC 581

RESULT 9

US-08-441-507-19
Sequence 19, Application US/08441507
Patent No. 6214358
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species Cynodon
TITLE OF INVENTION: Dactylon
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,507
FILING DATE: 15-May-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,875
FILING DATE: 30-October-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-049DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-441-507-19

Query Match      26.1%; Score 76; DB 3; Length 832;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGGGAAGACGCTGGTCTGAACATC 60
Db 296 ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAACGACCACTTACCTGGCGCTGCTCGTC 355
QY 61 AAGTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGGCAGCAGCGGCTCGGAG 120
Db 356 AAGTACGCGCGGGGATGGCAACATTGTGCGCGTGCACATCAAGCCCAAGGATCCGAC 415
QY 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 416 GAGTTCAATTCCTCCATGAAGTCTGCTGGGGGCCATCTGGAGGATCGACCCCAAGAGCCG 475
QY 178 CTCACCGGCCCAATGAACCTTCCGCTTCTCTCAAGGGCGGCATGAAGACGTTCTCGAC 237
Db 476 CTCAGGGGCCCTTCTCCATCCGCTCACCTCCGAGGGCGGCCCATCTCGTCCAGGAC 535
QY 238 GAGGTCAATCCCAACCGCTTCAAGGTTCGCGCAAAACCTACACCCC 281
Db 536 GAGTCAATCCAGCAACTGGAAGCCAGACACCGTCTACACCTC 579

RESULT 10
US-07-969-875A-19
; Sequence 19, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Knox, Robert B.;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A..
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-969-875A-19

Query Match      26.1%; Score 76; DB 3; Length 832;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGGGAAGACGCTGGTCTGAACATC 60
Db 296 ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAACGACCACTTACCTGGCGCTGCTCGTC 355
QY 61 AAGTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGGCAGCAGCGGCTCGGAG 120
Db 356 AAGTACGCGCGGGGATGGCAACATTGTGCGCGTGCACATCAAGCCCAAGGATCCGAC 415
QY 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 416 GAGTTCAATTCCTCCATGAAGTCTGCTGGGGGCCATCTGGAGGATCGACCCCAAGAGCCG 475
QY 178 CTCACCGGCCCAATGAACCTTCCGCTTCTCTCAAGGGCGGCATGAAGACGTTCTCGAC 237
Db 476 CTCAGGGGCCCTTCTCCATCCGCTCACCTCCGAGGGCGGCCCATCTCGTCCAGGAC 535
QY 238 GAGGTCAATCCCAACCGCTTCAAGGTTCGCGCAAAACCTACACCCC 281
Db 536 GAGTCAATCCAGCAACTGGAAGCCAGACACCGTCTACACCTC 579

RESULT 11
US-08-413-974-3
; Sequence 3, Application US/08413974
; Patent No. 6180368
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180368ris
; STREET: 1 Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,974
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,861
; FILING DATE:
; APPLICATION NUMBER: US/07/746,703
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-969-875A-19
```

MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE: Lolium perenne
FEATURE:
NAME/KEY: CDS
LOCATION: 3...437
US-08-413-974-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGGAGAAGGGTTCTGACGCGAAGACGCTGGTCTGAACATCAAGTACAGAGGCCAGGG 78
DB 168 GTGAGAAGGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGGCGAC 227
QY 79 GACACCTCGCGAGGTGAGCTCCGGCAGCAGCGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGTGTGGCCGTGGACATCAAGGAGAGGGCAAGATAAGTGGATCGAGCTCAAG 287
QY 136 ACGAAGAAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCCATTCACC 347
QY 196 TTCGGCTTCTCTTCAAGGGCGCATGAAGAAAGTCTTCGACGAGGTCAATCCCAACCGCC 255
DB 348 GTCCGCTACACCAACCGAGGGCGCACAAATCCGAAGTCGAGGATGTCTATCTCTGAGGGC 407
QY 256 TTCACGGTGGCAAAACCTACACCCCAAGT 286
DB 408 TGGAGGGCGACACCTCTACTCGGCCAAGT 438

RESULT 12
US-08-434-418-3
Sequence 3, Application US/08434418
Patent No. 6197313
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir et al.
TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
FILE REFERENCE: IMI-051CND2
CURRENT APPLICATION NUMBER: US/08/434,418
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: 08/202,861
PRIOR FILING DATE: 1994-25-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 756
TYPE: DNA
ORGANISM: Lolium perenne
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(437)
US-08-434-418-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGGAGAAGGGTTCTGACGCGAAGACGCTGGTCTGAACATCAAGTACAGAGGCCAGGG 78
DB 168 GTGAGAAGGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGGCGAC 227
QY 79 GACACCTCGCGAGGTGAGCTCCGGCAGCAGCGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGTGTGGCCGTGGACATCAAGGAGAGGGCAAGATAAGTGGATCGAGCTCAAG 287
QY 136 ACGAAGAAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCCATTCACC 347
QY 196 TTCGGCTTCTCTTCAAGGGCGCATGAAGAAAGTCTTCGACGAGGTCAATCCCAACCGCC 255

DB 348 GTCCGCTACACCAACCGAGGGCGCACAAATCCGAAGTCGAGGATGTCTATCTCTGAGGGC 407
QY 256 TTCACGGTGGCAAAACCTACACCCCAAGT 286
DB 408 TGGAGGGCGACACCTCTACTCGGCCAAGT 438

RESULT 13
US-08-433-288-3
Sequence 3, Application US/08433288
Patent No. 6239269
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir et al.
TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
FILE REFERENCE: IMI-051CND1
CURRENT APPLICATION NUMBER: US/08/433,288
CURRENT FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: 08/413,947
PRIOR FILING DATE: 1995-03-30
PRIOR APPLICATION NUMBER: 08/202,861
PRIOR FILING DATE: 1994-02-25
PRIOR APPLICATION NUMBER: 07/746,703
PRIOR FILING DATE: 1991-08-16
PRIOR APPLICATION NUMBER: 07/585,086
PRIOR FILING DATE: 1990-10-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 756
TYPE: DNA
ORGANISM: Lolium perenne
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(437)
US-08-433-288-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGGAGAAGGGTTCTGACGCGAAGACGCTGGTCTGAACATCAAGTACAGAGGCCAGGG 78
DB 168 GTGAGAAGGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGGCGAC 227
QY 79 GACACCTCGCGAGGTGAGCTCCGGCAGCAGCGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGTGTGGCCGTGGACATCAAGGAGAGGGCAAGATAAGTGGATCGAGCTCAAG 287
QY 136 ACGAAGAAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCCATTCACC 347
QY 196 TTCGGCTTCTCTTCAAGGGCGCATGAAGAAAGTCTTCGACGAGGTCAATCCCAACCGCC 255
DB 348 GTCCGCTACACCAACCGAGGGCGCACAAATCCGAAGTCGAGGATGTCTATCTCTGAGGGC 407
QY 256 TTCACGGTGGCAAAACCTACACCCCAAGT 286
DB 408 TGGAGGGCGACACCTCTACTCGGCCAAGT 438

RESULT 14
US-08-174-739A-3
Sequence 3, Application US/08174739A
Patent No. 6265566
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjoglou, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn

;; TITLE OF INVENTION: Ryegrass Pollen Allergen
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lahive & Cockfield, LLP
;; STREET: 60 State Street, Suite 510
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/174,739A
;; FILING DATE: 29-DEC-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: IMI-051DV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 756 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; ORIGINAL SOURCE: Lolium perenne
;; ORGANISM: Lolium perenne
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..437
US-08-174-739A-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAAGTACACGAGGCCAGGG 78
DB 168 GTCGAGAGAGGGTTCCAAACCCCAACTACTCTGGCTATTCTGGTGAAGTACGTGACGCGCAC 227

QY 79 GACACCCCTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGAGTGG---GAACCCCATG 135
DB 228 GCGCAGCTGGTGGCGGTGGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGCTCACCGGCCCAATGAAC 195
DB 288 GAGTCGTGGGAGCAGTCTGGAGGATCGACACCCCGGATAAGCTGACGGGCCCATTCACC 347

QY 196 TTCGCTTCTCTCCAAAGGGCGGCATGAAGACGCTTCGACGAGGTCTATCCCCACCGCC 255
DB 348 GTCCGCTACACCAAGGGCGGCACCAATCCGAAGTCGAGGATGTCTATCTCTGAGGCG 407

QY 256 TTCACGGTCGGCAAAACCTACACCCCAAGAT 286
DB 408 TGAAGGCCGACACCTCTACTCGGCCAAGT 438

RESULT 15
US-08-434-256-3
; Sequence 3, Application US/08434256
; Patent No. 6451324
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir, Knox, Robert B., Smith, Penelope,
; APPLICANT: Avjoglou, Asil, Theerakulpisut, Piyada, Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 25

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6451324ris
;; STREET: 1 Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/434,256
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hohenschutz, Liza D.
;; REGISTRATION NUMBER: 33,712
;; REFERENCE/DOCKET NUMBER: IMPH-0003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3949
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 756 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; ORIGINAL SOURCE: Lolium perenne
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..437
US-08-434-256-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAAGTACACGAGGCCAGGG 78
DB 168 GTCGAGAGAGGGTTCCAAACCCCAACTACTCTGGCTATTCTGGTGAAGTACGTGACGCGCAC 227

QY 79 GACACCCCTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGAGTGG---GAACCCCATG 135
DB 228 GCGCAGCTGGTGGCGGTGGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGCTCACCGGCCCAATGAAC 195
DB 288 GAGTCGTGGGAGCAGTCTGGAGGATCGACACCCCGGATAAGCTGACGGGCCCATTCACC 347

QY 196 TTCGCTTCTCTCCAAAGGGCGGCATGAAGACGCTTCGACGAGGTCTATCCCCACCGCC 255
DB 348 GTCCGCTACACCAAGGGCGGCACCAATCCGAAGTCGAGGATGTCTATCTCTGAGGCG 407

QY 256 TTCACGGTCGGCAAAACCTACACCCCAAGAT 286
DB 408 TGAAGGCCGACACCTCTACTCGGCCAAGT 438

Search completed: February 17, 2006, 19:13:49
Job time : 146 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: February 17, 2006, 17:09:48 ; Search time 472 Seconds
(without alignments)
4108.952 Million cell updates/sec
Title: US-10-628-296A-1
Perfect score: 291
Sequence: 1 acaaaagtcgatttaactgt.....cctacacccagaatacaat 291
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	100.0	291	12	ADJ65065
2	289.4	99.5	291	12	ADJ65067
3	150.2	51.6	3356	14	ADW43399
4	121.4	41.7	525	2	AAQ77731
5	90.2	31.0	611	11	ACL32712
6	82.6	28.4	1097	13	ADX31037
7	82.2	28.2	720	6	ABK48598
8	82.2	28.2	723	2	AAQ73599
9	82.2	28.2	723	2	AAQ73598
10	80.6	27.7	723	6	ABA95773
11	80.6	27.7	795	6	ABA95772
12	80	27.5	804	11	ACL30460
13	79.2	27.2	1072	2	AAQ65408
14	79.2	27.2	1253	13	ADX51373
15	79	27.1	723	2	AAQ73597
16	77.6	26.7	802	2	AAQ43054
17	76	26.1	759	2	AAQ43056
18	76	26.1	775	2	AAQ43050
19	76	26.1	832	2	AAQ43055

20	74.2	25.5	723	12	ADM81042
21	72.6	24.9	1035	4	AAQ89427
22	69.4	23.8	810	2	AAQ22246
23	69.4	23.8	1123	2	AAQ65409
24	69.4	23.8	1124	2	AAQ73596
25	68.8	23.6	662	2	AAQ43049
26	68.6	23.6	306	6	ABL74807
27	67.2	23.1	594	2	ABL74807
28	66.8	23.0	807	11	ACL34470
29	66.8	23.0	807	12	ADJ44775
30	66.8	23.0	1029	13	ADX31184
31	66.8	23.0	1047	13	ADX54257
32	66.8	23.0	1062	13	ADX30070
33	66.2	22.7	801	11	ACL30260
34	66.2	22.7	804	11	ACL26583
35	65	22.3	609	13	ADX09301
36	65	22.3	1273	8	AD49517
37	62	21.3	969	13	ADX34895
38	61.6	21.2	1170	13	ADR73684
39	61.2	21.0	330	12	ADJ39720
40	61.2	21.0	2000	8	ADA72433
41	60.4	20.8	1089	13	ADX35044
42	59	20.3	1401	13	ADT19043
43	58	19.9	354	12	ADJ39535
44	57	19.6	1164	13	ADT19962
45	57	19.6	1200	13	ADX54116

ALIGNMENTS

RESULT 1
ADJ65065
ID ADJ65065 standard; cDNA; 291 BP.
XX
AC ADJ65065;
XX
DT 06-MAY-2004 (first entry)
XX
DE Ryegrass Lol p 3 allergen encoding cDNA SEQ ID NO:1.
XX
KW allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
KW ryegrass; Lol p 3; gene; ss.
XX
OS Lolium perenne.
XX
FH Key Location/Qualifiers
FT CDS 1..291
FT FT /*tag= a
FT FT /product= "Ryegrass Lol p 3 allergen"
XX
PN WO2004011025-A1.
XX
PD 05-FEB-2004.
XX
28-JUL-2003; 2003WO-US023600.
XX
PR 29-JUL-2002; 2002US-0399688P.
XX
(PENN-) PENN STATE RES FOUND.
XX
Li L, Cosgrove D;
XX
WPI; 2004-143737/14.
DR P-PSDB; ADJ65066.
XX
PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.
XX
PS Claim 1; SEQ ID NO 1; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (I); (2) a vector (III) comprising (II); (3) a host cell comprising (III); (4) a group of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I); (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing into a plant an expression cassette comprising a promoter active in cells of plants operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (8) a method of producing a polypeptide having expansin activity; (9) a method for cell wall comprising a nucleic acid that comprises S1; (11) a transgenic plant with a genome comprising a nucleic acid that comprises S1 and that possesses expansin activity, or a transgenic plant comprising an expression cassette operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; and (12) seeds of the plant described above, which carry the DNA construct in their genome. (I) has plant growth regulant activity, and can be used in gene therapy. The composition and methods of the present invention can be used in altering plant cell wall properties, which may effect growth, flexibility and mechanical strength in tissues in which they are expressed. The present sequence encodes the ryegrass Lol p 3 allergen, which is used in the exemplification of the present invention.

XX Sequence 291 BP; 77 A; 83 C; 88 G; 43 T; 0 U; 0 Other;

Query Match 100.0%; Score 291; DB 12; Length 291;
 Best Local Similarity 100.0%; Pred. No. 7.6e-57;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGCTGTAACATC 60
 Db 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGCTGTAACATC 60

QY 61 AAGTACACGAGCCAGGGGACACCTCGCGAGGTGGAGCTCCGCGACAGCGCTCGGAG 120
 Db 61 AAGTACACGAGCCAGGGGACACCTCGCGAGGTGGAGCTCCGCGACAGCGCTCGGAG 120

QY 121 GAGTGGGAACCCATGACGAGAGGGCAACCTGTGGAGGTGAAGAGCGCAAGCCGCTC 180
 Db 121 GAGTGGGAACCCATGACGAGAGGGCAACCTGTGGAGGTGAAGAGCGCAAGCCGCTC 180

QY 181 ACCGGCCCAATGAATCTCCGCTTCTCTCCAGGGCGGCATGAAGACGTCTTCGACGAG 240
 Db 181 ACCGGCCCAATGAATCTCCGCTTCTCTCCAGGGCGGCATGAAGACGTCTTCGACGAG 240

QY 241 GTCAATCCCAACCGCTTCAAGTGGGCAAAACCTACACCCCAAGATACAAT 291
 Db 241 GTCAATCCCAACCGCTTCAAGTGGGCAAAACCTACACCCCAAGATACAAT 291

RESULT 2
 ADJ65067
 ID ADJ65067 standard; cDNA; 291 BP.
 XX
 AC ADJ65067;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Ryegrass Lol p 3 allergen modified variant cDNA SEQ ID NO:3.
 XX
 KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
 KW ryegrass; Lol p 3; modified; variant; gene; ss.
 XX
 OS Lolium perenne.
 OS Synthetic.

XX WO2004011025-A1.
 XX
 XX PD 05-FEB-2004.
 XX
 XX PF 28-JUL-2003; 2003WO-US023600.
 XX
 XX PR 29-JUL-2002; 2002US-0399688P.
 XX
 XX PA (PENN-) PENN STATE RES FOUND.
 XX
 XX PI Li L, Cosgrove D;
 XX WPI; 2004-143737/14.
 XX
 XX New isolated nucleic acid molecules encoding polypeptides having expansin activity, useful for altering plant cell wall properties to effect growth, flexibility and mechanical strength in tissues in which they are expressed.

XX Disclosure; SEQ ID NO 3; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (I); (2) a vector (III) comprising (II); (3) a host cell comprising (III); (4) a group of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I); (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing into a plant an expression cassette comprising a promoter active in cells of plants operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (8) a method of weakening the mechanical strength of cellulose fibres; (9) a method for producing a polypeptide having expansin activity; (10) a transgenic plant cell comprising a nucleic acid that comprises S1; (11) a transgenic plant with a genome comprising a nucleic acid that comprises S1 and that possesses expansin activity, or a transgenic plant comprising an expression cassette operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (12) seeds of the plant described above, which carry the DNA construct in their genome. (I) has plant growth regulant activity, and can be used in gene therapy. The composition and methods of the present invention can be used in altering plant cell wall properties, which may effect growth, flexibility and mechanical strength in tissues in which they are expressed. The present sequence represents a modified variant ryegrass Lol p 3 allergen cDNA sequence, which is used in the exemplification of the present invention.

XX Sequence 291 BP; 76 A; 84 C; 88 G; 43 T; 0 U; 0 Other;

Query Match 99.5%; Score 289.4; DB 12; Length 291;
 Best Local Similarity 99.7%; Pred. No. 1.8e-56;
 Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGCTGTAACATC 60
 Db 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGCTGTAACATC 60

QY 61 AAGTACACGAGCCAGGGGACACCTGTGGAGGTGGAGCTCCGCGACAGCGCTCGGAG 120
 Db 61 AAGTACACGAGCCAGGGGACACCTGTGGAGGTGGAGCTCCGCGACAGCGCTCGGAG 120

QY 121 GAGTGGGAACCCATGACGAGAGGGCAACCTGTGGAGGTGAAGAGCCCAAGCCGCTC 180
 Db 121 GAGTGGGAACCCATGACGAGAGGGCAACCTGTGGAGGTGAAGAGCCCAAGCCGCTC 180

QY 181 ACCGGCCCAATGAATCTCCGCTTCTCTCCAGGGCGGCATGAAGACGTCTTCGACGAG 240
 Db 181 ACCGGCCCAATGAATCTCCGCTTCTCTCCAGGGCGGCATGAAGACGTCTTCGACGAG 240

QY 241 GTCATCCCGCCGCTTACCGTGGCAAAACCTACACCCAGATAACAAT 291
 |||||
 Db 241 GTCATCCCGCCGCTTACCGTGGCAAAACCTACACCCAGATAACAAT 291

RESULT 3

ID ADW43399 standard; DNA; 3356 BP.
 XX ADW43399;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Perennial ryegrass Lol p 2 genomic DNA, SEQ ID NO:1.
 XX
 KW Transgenic plant; pollen; male infertility; immunogenicity; plant;
 XX allergen; Lol p 2; gene; ds.
 XX
 OS Lolium perenne; cv. Barlano.
 XX
 FH Key Location/Qualifiers
 FT promoter 1..2789
 FT /tag= a
 FT /note= "Corresponds to SEQ ID NO:2"
 FT complement(1704..1723)
 FT primer_bind
 FT /tag= b
 FT /note= "Binds primer D21pr1L (SEQ ID NO:7)"
 FT promoter 1837..2789
 FT /tag= c
 FT /note= "Corresponds to SEQ ID NO:3"
 FT complement(2772..2798)
 FT primer_bind
 FT /tag= d
 FT /note= "Binds primer D21pr1R (SEQ ID NO:8)"
 FT CDS 2790..3155
 FT /tag= e
 FT /product= "Lol p 2 protein"
 FT 3202..3204
 FT misc_signal
 FT /tag= f
 FT /note= "Additional stop codon"
 FT misc_signal 3206..3208
 FT /tag= g
 FT /note= "Additional stop codon"
 FT misc_signal 3271..3273
 FT /tag= h
 FT /note= "Additional stop codon"
 FT misc_signal 3330..3332
 FT /tag= i
 FT /note= "Additional stop codon"
 FT misc_signal 3340..3342
 FT /tag= j
 FT /note= "Additional stop codon"
 FT misc_signal 3351..3353
 FT /tag= k
 FT /note= "Additional stop codon"
 FT
 FN WO2004113536-A1.
 PN
 XX
 PD 29-DEC-2004.
 XX
 PF 18-JUN-2004; 2004WO-AU000802.
 XX
 PR 20-JUN-2003; 2003AU-00903132.
 XX
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.
 XX
 PI Spangenberg G, Lidgett AJ, Petrovska N, Emmerling M;
 XX
 DR WPI; 2005-048831/05.
 XX
 XX New isolated nucleic acid molecule capable of modifying pollen-specific
 PT expression, useful in plant breeding and development, in particular for
 PT producing transgenic plants with desired phenotypes.
 XX

PS Example 1; SEQ ID NO 1; 46pp; English.
 XX
 CC The invention relates to isolated promoter sequences (ADW43400 and
 CC ADW43401) from the perennial ryegrass pollen allergen Lol p 2 gene which
 CC are capable of modifying pollen-specific expression. The invention also
 CC relates to vectors comprising a Lol p 2 promoter sequence; chimeric genes
 CC comprising a Lol p 2 promoter operably linked to a second nucleic acid,
 CC particularly one which downregulates pollen allergen expression; and
 CC plant cells, plants, plant seeds or other plant tissues comprising an
 CC isolated Lol p 2 promoter or vectors or chimeric genes comprising a Lol p
 CC 2 promoter. The Lol p 2 promoter sequences and vectors and chimeric genes
 CC containing them can be used to modify gene expression in pollen or to
 CC modify pollen-specific expression. Vectors and chimeric genes comprising
 CC a Lol p 2 promoter sequence operably linked to a polynucleotide which
 CC downregulates the expression of pollen allergen genes (e.g., Lol p 1 or
 CC Lol p 2 antisense sequences) can be used to generate low allergy plants.
 CC Alternatively, a Lol p 2 promoter sequence can be operably linked to a
 CC gene capable of modulating male fertility; such constructs are useful in
 CC producing plants with reduced male fertility, or for restoring male
 CC fertility in male-sterile plants. The present sequence represents a 3.3
 CC kb genomic Lol p 2 sequence comprising an approximately 2.7 kb 5'
 CC promoter region (ADW43400) and a 366 bp open reading frame encoding a 121
 CC residue protein. This sequence was obtained from a 3.9 kb genomic clone
 CC isolated by hybridization screening of a Lambda-DASH l0ium perenne cv.
 CC Barlano genomic library with a Lol p 2 cDNA sequence.
 XX
 SQ Sequence 3356 BP; 939 A; 808 C; 774 G; 831 T; 0 U; 4 Other;
 Query Match 51.6%; Score 150.2; DB 14; Length 3356;
 Best Local Similarity 74.2%; Pred. No. 1.le-24;
 Matches 204; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
 QY 13 TTAACCTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGGCTGAACATCAAGTACACGAGG 72
 Db 2874 TTCACGTAGAGAGGGCTCCGACGAGAGACCTGGCGCTGTCATCAAGTACACACAG 2933
 QY 73 CCAGGGGACACCTTGGCGAGGTGAGCTCCGGGACGACGCTCGGAGAGGTGGGAACCC 132
 Db 2934 GAGGGCGACTCCATGGCGAGGTGGAGCTCAAGGAGCAGCGCTCCAAACGAGTGGTGGCC 2993
 QY 133 ATGACGAGAGAGGGCAA---CCTGTGGGAGGTGAAGAGCGCCCAAGCCGCTCACCGGCCCA 189
 Db 2994 CTGAAGAAGAACGCGCAGCGCGTGTGGGAGATCAAGAGCGACAAAGCCGCTCAAGGGGCCA 3053
 QY 190 ATGAACCTTCGCTTCTCTCCAAGGGCGCATGAAGAAGCTTTCGACGAGGTCTATCCCC 249
 Db 3054 TTCAACTTCCGCTTCGTGTCCGAGNAGGGGATGAGGAACGTGTCGACGACGTGGTTCGG 3113
 QY 250 ACCGCTTTCACGGTCCGCAAAACCTTACACCCCGAGA 284
 Db 3114 GCGGAGTTCAAGGTGCGCACCCACCTTACAAGGCCGA 3148
 RESULT 4
 ID AAQ77731 standard; cDNA; 525 BP.
 XX
 AC AAQ77731;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-JUN-1995 (first entry)
 XX
 DE Recombinant timothy grass allergen Phl pII DNA sequence.
 XX
 KW Timothy grass; Phleum pratense; allergen; recombinant; group II/III;
 KW grass; plant; pollen; B-cell; T-cell; epitope; detection; allergy; ss.
 XX
 OS Phleum pratense.
 XX
 FH Key Location/Qualifiers
 FT CDS 25..393
 FT /tag= a
 FT /product= "Phl pII allergen"
 FT

Db 555 GACGTCATCCCAAGGGCTGGAAGCGGACACCTCTCTAC 593
ADX31037
ID ADX31037 standard; cDNA; 1097 BP.
XX
AC ADX31037;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 13857.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 13857; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1097 BP; 272 A; 290 C; 308 G; 227 T; 0 U; 0 Other;
Query Match 28.4%; Score 82.6; DB 13; Length 1097;

Best Local Similarity 57.8%; Pred. No. 2.4e-09;
Matches 167; Conservative 0; Mismatches 119; Indels 3; Gaps 1;
QY 2 CAAGAAGTGTAACTGTGGAGAGGGTCTCTGACGCGAAGACGCTGGTGTGAACATCA 61
DB 543 CCAAGGTACCTTCCACCTTGAAGAGGGTGGCGGCCCACTACCTGGCAGCTGTGGTCA 602
QY 62 AGTACACGAGGCCAGGGGACACCTCTGGCGAGGTGGAGCTCCGCGAGCAGCGGCTCGGAGG 121
DB 603 AGTACGTGACGGCGACGGTGCATTTGTGGCAGTGGACGTCAAGGAGAGGGCTCCGACA 662
QY 122 AGTGGGAACCCATGAGGAAGA---AGGGCAACTCTGTGGAGGTGAAGAGCGCCCAAGCCGC 178
DB 663 CGTACGAGCCTCTGAAGCAGCTCTGGGGCGCCATCTGGAGGAAGGACAGCGCAAAACCGC 722
QY 179 TCACCGGGCCCAATGAACCTTCCGCTCTCTCAAGGGCGGCATGAAGAACGCTTCTCGAGC 238
DB 723 TTAAGGAGCCCTTCAACGCTCCGCTCACTACGAGGGAGGACCAAGTCCGCTACGAGC 782
QY 239 AGGTTCATCCCCACCGCCTTTCACGCTCGGCAAAACCTACACCCCGAGAATA 287
DB 783 ATGTCATCCTCGCAACTTGAAGGCCAACACCGCCTACACCGCCAAATA 831
RESULT 7
ABK48598
ID ABK48598 standard; cDNA; 720 BP.
XX
AC ABK48598;
XX
DT 02-JUL-2002 (first entry)
XX
DE Hypoallergenic variant of the Phleum pratense allergen, Phl p 1, cDNA.
XX
KW Plant; ss; gene; Gramineae; hypoallergenic; allergen; Phl p 1; pollen;
KW immunotherapy; beta-expansin; hypersensitising immunotherapy; SIR;
KW vaccine; allergic disease; bronchial asthma; allergic rhinitis;
KW allergic dermatitis; allergic conjunctivitis; antiallergic;
KW antiasthmatic; antiinflammatory; dermatological.
XX
OS Phleum pratense.
XX
FH Key Location/Qualifiers
FT CDS 1..720
FT /tag= a
FT /product= "Phl p 1 allergen"
FT /partial
FT /note= "No start or stop codon"
XX
PN WO200222679-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-EP010485.
XX
PR 12-SEP-2000; 2000IT-MI001987.
XX
PA (CNDR) CONSIGLIO NAZ DELLE RICERCHE.
XX
PI Sturaro M, Viotti A, Falagiani P, Mistrello G, Roncarolo D;
PI Zanotta S;
XX
DR WPI; 2002-351877/38.
DR P-PSDB; AU79518.
XX
PT Novel variant of class 1 allergenic protein Phl p1 of Gramineae, useful
PT in the prophylactic and therapeutic treatment of allergic diseases.
XX
PS Claim 8; Page 13; 14pp; English.
XX
CC The invention discloses a variant of the pollen/class 1 allergenic
CC protein, Phl p1, of Gramineae, such as Phleum pratense, where at least
CC one of the Lys residues present at the positions 28, 35, 44, 48, 179, 181,

XX (IMMU-) IMMULOGIC PHARM CORP.
 XX Griffith IJ, Kuo M, Luqman M, Powers S;
 XX WPI: 1994-316937/39.
 XX P-PSDB; AAR60705.
 XX Isolated peptide(s) of Lol or p I, major protein allergen of species
 PT Lolium perenne. - useful for diagnosis and treatment of sensitivity to
 PT rye-grass pollen allergen.
 XX Example 5; Fig 6; 125pp; English.
 XX AAQ73598 is the PCR generated full length clone 114, which encodes Poa pi
 CC (AAR60705) a major protein allergen of Poa pratensis. Internal peptides
 CC (AAR60710-R60757) isolated from a ryegrass major protein antigen
 CC (AAR60703) can be used in the treatment and diagnosis of sensitivity to
 CC ryegrass pollen protein (Lol pi), or pollen proteins that are
 CC immunologically related to Lol pi e.g. Dac g1, Phl pi and Poa pi.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC Revised record issued on 21-OCT-2004 : Correction to feature table key
 XX Sequence 723 BP; 156 A; 242 C; 233 G; 90 T; 0 U; 2 Other;

Query Match 28.2%; Score 82.2; DB 2; Length 723;
 Best Local Similarity 58.4%; Pred. No. 2.8e-09;
 Matches 163; Conservative 0; Mismatches 113; Indels 3; Gaps 1;
 QY 1 ACAAAAGTCGATTAACTGTGAGAGGGTTCTGACGGGAAGACGCTGGTGTGAACATC 60
 DB 433 ACCAAGGTACCTTCCACGTGAGAGGGGTTCCAAACCCCACTACCTTGGCTGTGGTG 492
 QY 61 AAGTACACGAGCCAGGGAGACACCTTGGCGGAGGTGGAGCTCGGCAGACGCTCGGAG 120
 DB 493 AAGTACGTGACGCGGACGGGACGCTGGTGGCGGTGGACATCAAGCAGAAGGGCAAGGAC 552
 QY 121 GAGTGG---GAACCATGACGAAGAGGGCAACCTGTGGGAGGTGAAGAGCCCAAGCCG 177
 DB 553 AAGTGGATCGAGCTCAAGAGTCTGGGGAGCGGCTTGGAGATCGACACCCCGACAG 612
 QY 178 CTCACCGGCCCAATGAACCTTCGCTTCTCTCAAGGGCGGCATGAAGAACGCTTTCGAC 237
 DB 613 CTCACGGGCCCTTACCGTCCGCTACACCAACCGAGGGGGCACCAAGCCGAGCCGAG 672
 QY 238 GAGGTATCCCCACCGCCTTACGGTCGGCAAAACCTAC 276
 DB 673 GACGTATCCCGAGGGCTGGAAGGCCGACACCGCCTAC 711

RESULT 10
 ABA95773
 ID ABA95773 standard; DNA; 723 BP.
 XX AC ABA95773;
 XX 05-APR-2002 (first entry)
 XX Orchard grass pollen allergen Dac g1 mature form coding sequence.
 DE Orchard grass; pollen; allergen; Dac g1; antiallergic; gene; allergy;
 KW plant; ds.
 XX Dactylis glomerata.
 OS Key Location/Qualifiers
 XX 1..723
 FT CDS /tag= a
 FT /product= "Mature Dac g1"
 FT
 XX PN FR2809415-A1.
 XX

PD 30-NOV-2001.
 XX 29-MAY-2000; 2000FR-00006856.
 XX 29-MAY-2000; 2000FR-00006856.
 XX (SETB) SOC NAT EXPL IND TABACS & ALLUMETTES.
 PA (STAL-) STALLERGENES.
 XX Van Ree R, Van Oort E, Bonneau C, Paye L, Gomord V;
 XX WPI: 2002-043466/06.
 DR P-PSDB; AAM48319.
 XX New nucleic acid encoding the allergen Dac g1 of Dactylis glomerata,
 PT useful for diagnosis and immunotherapy of allergy.
 XX Claim 3; Page 24-26; 29pp; French.
 XX The present sequence is the coding sequence for the mature form of the
 CC Dac g1 pollen allergen from orchard grass (Dactylis glomerata). Dac g1 is
 CC useful for treatment or diagnosis of allergy, particularly sensitivity to
 CC pollen from herbaceous plants, specifically Dactylis glomerata
 XX Sequence 723 BP; 165 A; 222 C; 242 G; 94 T; 0 U; 0 Other;
 SQ Query Match 27.7%; Score 80.6; DB 6; Length 723;
 Best Local Similarity 58.1%; Pred. No. 6.5e-09;
 Matches 162; Conservative 0; Mismatches 114; Indels 3; Gaps 1;
 QY 1 ACAAAAGTCGATTAACTGTGAGAGGGTTCTGACGGGAAGACGCTGGTGTGAACATC 60
 DB 433 ACCAAGGTGACCTTCCACGTGAGAGGGTTCACACCCCACTACCTTGGCTGTGGTG 492
 QY 61 AAGTACACGAGCCAGGGAGACACCTTGGCGGAGGTGGAGCTCGGCAGACGCTCGGAG 120
 DB 493 AAGTACGTGACGCGGACGGGACGCTGGTGGCGGTGGATATCAAGGAGAAGGGCAAGGAC 552
 QY 121 GAGTGGGAACCCATCAACGAAGAA---GGCAACCTGTGGGAGGTGAAGAGCGCAAGCCG 177
 DB 553 AAGTGGATCGCGCTCAAGAGTCTAGGGAGCCATCTGGAGGTGGACACACCCGACAG 612
 QY 178 CTCACCGGCCCAATGAACCTTCGCTTCTCTCAAGGGCGGCATGAAGAACGCTTTCGAC 237
 DB 613 CTCACGGGCCCTTACCGTCCGCTACACCAACCGAGGGGGCACCAAGTCCGGAAGTTGAG 672
 QY 238 GAGGTATCCCCACCGCCTTACGGTCGGCAAAACCTAC 276
 DB 673 GATGTATCCCGAGGGCTGGAAGGCCGACACCTCCTAC 711

RESULT 11
 ABA95772
 ID ABA95772 standard; DNA; 795 BP.
 XX AC ABA95772;
 XX 05-APR-2002 (first entry)
 XX Orchard grass pollen allergen Dac g1 proform coding sequence.
 DE Orchard grass; pollen; allergen; Dac g1; antiallergic; gene; allergy;
 KW plant; ds.
 XX Dactylis glomerata.
 OS Key Location/Qualifiers
 XX 1..795
 FT CDS /tag= a
 FT /product= "Dac g1"
 FT sig_peptide 1..72
 FT /tag= b
 FT mat_peptide 73..792


```
XX IgE; allergy; antigen; diagnosis; treatment; ss.
XX Sorghum halepense.
XX Key Location/Qualifiers
XX misc_feature 25..822
XX /tag= d
XX /note= "preferred fragment"
XX CDS 37..822
XX /tag= a
XX misc_feature 37..822
XX /tag= e
XX misc_feature 40..822
XX /note= "preferred fragment"
XX /tag= f
XX misc_feature 109..833
XX /note= "preferred fragment"
XX /tag= c
XX mat_peptide 109..822
XX /tag= b
XX WO9410314-A1.
XX 11-MAY-1994.
XX 29-OCT-1993; 93WO-AU000559.
XX 30-OCT-1992; 92US-00971096.
XX (UYME ) UNIV MELBOURNE.
XX Singh MB, Knox RB, Avijooglu A;
XX WPI; 1994-167469/20.
XX P-PSDB; AAR54949.
XX DNA encoding allergenic proteins and peptide(s) from Johnson grass pollen
XX allergen Sorhi - for diagnosing, treating and preventing allergy to
XX Johnson pollen.
XX Claim 4; Fig 5; 81pp; English.
XX The sequence is that of a cDNA clone encoding a Johnson grass pollen
XX allergen Sorhi obtd. by screening a S. halepense cDNA library with anti-
XX group I antibodies raised against ryegrass and Bermuda grass. The DNA can
XX be used for diagnosing, treating and preventing allergy to Johnson grass
XX pollen. See also AAQ65409-17. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Sequence 1072 BP; 258 A; 300 C; 322 G; 192 T; 0 U; 0 Other;

Query Match 27.2%; Score 79.2; DB 2; Length 1072;
Best Local Similarity 56.8%; Pred. No. 1.4e-08;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 3 AAAAGTCGATTTAACTGTGGAGAGGTTCTACCGGAGAGCGCTGGTCTGAACATCAA 62
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 537 AAAGTCACTTCCACGTGGAGAGGGGAGCAACCCCACTACCTGGCTCTGTGGTCAA 596
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 GTACACGAGGCCAGGGGACACCCCTCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGA 122
DB GTACCTGACGCGGACGGTGACGTTGTGGGGTGGACATCAAGAGAGAGGGTGGCGAGCG 656
QY 123 GTGGGAACCCATGACGAAGAA---GGGCACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCT 179
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 657 GTACCAGGCCCTCAAGCACTCTGGGGCGCTATCTGGAGGAGGACAGCGCAAGCCCAAT 716
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 CACCGGCCCATGAATCTCCGCTTCTCTCCAGAGCGCGCATGAAGAGCTTTTCGACGA 239
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 717 CAAGTTTCCCGTCACCGTCCCAATCACCACCGAGGGGAGCACCAGACCGCTCAGGAAGA 776
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 240 GGTCTATCCCAACCGCTTTCACGGTGGCGAAACCTACACCCGAGATACAAT 291
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 777 GGTCTATCCCAAGAGGCTGGAGGCGGACACCTACACCGCAATAAAT 828
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
ADXS1373
ID ADXS1373 standard; cDNA; 1253 BP.
XX AC ADXS1373;
XX DT 21-APR-2005 (first entry)
XX Plant full length insert polynucleotide seqid 26113.
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX OS Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX Claim 1; SEQ ID NO 26113; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX Sequence 1253 BP; 332 A; 327 C; 342 G; 252 T; 0 U; 0 Other;
```

Query Match 27.2%; Score 79.2; DB 13; Length 1253;
Best Local Similarity 56.8%; Pred. No. 1.4e-08;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
QY 3 AAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGGTGTGGTGAACATCAA 62
DB 551 AAAGTCACTTCCACGTTGAGAGAGGGGAGCAACCCCAACTACCTGCTGTGGTCAA 610
QY 63 GTACACGAGGCCAGGGACACCTGGCGAGGTGGAGCTCGGCGACGCGCTCGGAGGA 122
DB 611 GTACGTCGACGCGACGCGTGCCTGTGGGGGTGGACATCAAGGAGAGGGTGGCGAGC 670
QY 123 GTGGGAAACCCATGACGAAGAA---GGGCAACTGTGGGAGGTGAAGAGCGCAAGCCGCT 179
DB 671 GTACAGGCCCTCAAGCACTCTCTGGGGGGCTATCTGGAGGAGGACAGCGACAGCCAA 730
QY 180 CACCGGCCCAATGAATCTCCGCTTCTCTCCAAAGGGCGGCATGAAGAACGTTCTGACGA 239
DB 731 CAAGTTTCCCGTCAACGCTCAAAATCACCAACGAGGGAGGCCCAAGACCGCTACGAAGA 790
QY 240 GGTCAATCCCAACCGCTTCAAGTCCGCAAAACCTACACCCAGATACAAAT 291
DB 791 CGTCATCCCGAAGGCTGGAGGCGGACACCACTTACACCGCCCAATAAAT 842

RESULT 15

AAQ73597 standard; cDNA; 723 BP.

XX AC AAQ73597;
XX DT 25-MAR-2003 (revised)
XX DT 01-JUN-1995 (first entry)
XX DE Dactylis glomerata protein allergen (Dac gl) cDNA clone 106.5.
XX KW Dactylis glomerata protein allergen; Dac gl; ryegrass pollen allergen;
XX LW Lol pI; Poa pI; Phl pI; ss.
XX OS Dactylis glomerata.

Key Location/Qualifiers
FT mat_peptide 1..720
FT /tag= a

W09421675-A2.

29-SEP-1994.

09-MAR-1994; 94WO-US002537.

12-MAR-1993; 93US-00031001.

(IMMU-) IMMULOGIC PHARM CORP.

Griffith LJ, Kuo M, Luqman M, Powers S;

WPI; 1994-316937/39.

P-PSDB; AAR60704.

Isolated peptide(s) of Lol or p I, major protein allergen of species
Lolium perenne.- useful for diagnosis and treatment of sensitivity to
rye-grass pollen allergen.

Example 5; Fig 5; 125pp; English.

AAQ73597 is the PCR generated full length clone 106.5, which encodes Dac
gl (AAR60704) a major protein allergen of Dactylis glomerata. Internal
peptides (AAR60710-R60757) isolated from a ryegrass major protein antigen
(AAR60703) can be used in the treatment and diagnosis of sensitivity to
ryegrass pollen protein (Lol pI), or pollen proteins that are
immunologically related to Lol pI e.g. Dac gl, Phl pI and Poa pI.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 723 BP; 160 A; 220 C; 248 G; 95 T; 0 U; 0 Other;
SQ Matches 161; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

Query Match 27.1%; Score 79; DB 2; Length 723;
Best Local Similarity 57.7%; Pred. No. 1.5e-08;
Matches 161; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 1 ACAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGCTGCTGAACATC 60
DB 433 ACCAAGGTGACCTTCCACGTCGAGAGGGTTCCAAACCCCACTACTCTGGCGCTGCTGGTG 492
QY 61 AAGTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGGGAGCACGGCTCGGAG 120
DB 493 AAGTACGTCGACGCGGACGCGACGCTGTGGCGGTGGATATCAAGGAGAGGGCAAGGAC 552
QY 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
DB 553 AAGTGSATCGCGCTCAAGGAGTCATGGGGAGCCATCTGGAGGGTGGACACCCCGCAAG 612
QY 178 CTCAACCGGCCCCAATGAATCTCCGCTTCTCTCCAAAGGGCGGCATCAAGAAAGTCTTTCGAC 237
DB 613 CTGACGGGCCCATTTCAACGTTCTGCTACACCAACCGGGGAGGACCAACAGTCCGAAAGTTGAG 672
QY 238 GAGTCAATCCCAACCGCTTTCACGCTCGGCAAAACCTAC 276
DB 673 GACGTCATCCCGGAGGCTGGAGGCGGACGCCAGCTAC 711

Search completed: February 17, 2006, 17:17:57

Job time : 476 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 17:18:13 ; Search time 3002 Seconds

(without alignments)

5510.141 Million cell updates/sec

Title: US-10-628-296A-1

Perfect score: 291

Sequence: 1 acaaaagtcgatttaactgt.....cctacacccagaatacaat 291

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	100.0	291	15	AV135645 Lolium pe
2	227	78.0	294	15	AY421969 Phleum pr
3	223.4	76.8	291	15	DG025343 Dactylis gl
4	189.6	65.2	616	15	Z50867 T.aestivum
5	129.4	44.5	369	15	CDAL13135
6	129.2	44.4	264	15	LPOLPLI
7	126.2	43.4	369	15	DGL131334
8	126.2	43.4	369	15	HLA131336
9	126.2	43.4	369	15	LIT131339
10	126.2	43.4	369	15	PPR131337
11	126.2	43.4	369	15	TAE131338
12	126.2	43.4	525	15	PPPHLP1
13	121.4	41.7	369	6	A40218
14	93	32.0	137065	14	AC149815
15	88.6	30.4	825	15	AY543539
16	87	29.9	792	15	HLA012714
17	82.2	28.2	496	15	AY533100
18	82.2	28.2	720	6	AX405222

19	82.2	28.2	1066	15	PPPHLP1	X78813 P.pratense
20	82.2	28.2	1111	15	AY533101	AY533101 Triticum
21	82.2	28.2	1149	15	AY533103	AY533103 Triticum
22	81	27.8	792	15	PPR131850	AJ131850 Poa prate
23	80.6	27.7	723	6	AX323111	AX323111 Sequence
24	80.6	27.7	795	6	AX323109	AX323109 Sequence
25	80.6	27.7	795	15	AY241677	AY241677 Dactylis
26	80.6	27.7	960	15	AY543540	AY543540 Triticum
27	80	27.5	1164	15	AK072792	AK072792 Oryza sat
28	80	27.5	1254	15	AF261270	AF261270 Oryza sat
29	80	27.5	3381	15	AY039023	AY039023 Oryza sat
30	80	27.5	110000	15	AF008209_003	Continuation (4 of
c 31	80	27.5	110000	15	AF008209_003	Continuation (4 of
32	80	27.5	137033	15	AC107224	AC107224 Oryza sat
c 33	80	27.5	137033	15	AC107224	AC107224 Oryza sat
34	79.2	27.2	1072	6	I16888	I16888 Sequence 1
35	79.2	27.2	1072	6	I76296	I76296 Sequence 1
36	79	27.1	723	15	AY241676	AY241676 Dactylis
37	79	27.1	1086	15	HLHOLLIGN	Z68893 H.lanatus m
38	79	27.1	1141	15	HLHOLLIGN	Z27084 H.lanatus m
39	78.6	27.0	1068	15	AY533102	AY533102 Triticum
40	78.6	27.0	1088	15	S80654	S80654 major aller
41	78.6	27.0	1216	15	AY533104	AY533104 Triticum
42	78.4	26.9	3501	15	AF391106	AF391106 Oryza sat
43	77.6	26.7	802	6	AR225155	AR225155 Sequence
44	77.4	26.6	1152	15	PPPHLP1X	Z27090 P.pratense
45	76	26.1	759	6	AR225157	AR225157 Sequence

ALIGNMENTS

RESULT 1	AY135645	291 bp	DNA	linear	PLN 23-JAN-2003
LOCUS	Lolium perenne grass pollen allergen Lol p 3 gene, partial cds.				
DEFINITION	AY135645				
ACCESSION	AY135645				
VERSION	AY135645.1	GI:27883900			
KEYWORDS					
SOURCE	Lolium perenne				
ORGANISM	Lolium perenne				

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poace; Lolium.

REFERENCE 1 (bases 1 to 291)
Li,L.-C., Shieh,M.W. and Cosgrove,D.J.
Group 2, and group 3 allergens of grass pollen have plant cell wall-loosening activity characteristic of beta-expansins
Unpublished

REFERENCE 2 (bases 1 to 291)
Li,L.-C., Shieh,M.W. and Cosgrove,D.J.
Direct Submission

TITLE Submitted (24-JUL-2002) Biology, Penn State University, 208 Mueller Lab, University Park, PA 16802, USA

FEATURES
Location/Qualifiers

source
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/organism="Lolium perenne"
/mol_type="genomic DNA"
/db_xref="taxon:4522"
<1..>291
/product="grass pollen allergen Lol p 3"
<1..>291
/codon_start=1
/product="grass pollen allergen Lol p 3"
/protein_id="AA12883.1"
/db_xref="GI:27883901"
/translation="TKVGLTVKSGDAKTLVNLNKYTRPGDTLAEVLRHQHSEMEP
MTKGNLNEVKSAPLITGPMNFRFLSKGMKNVDFEIVTFTVGTGYTPEYN"

ORIGIN

Query Match 100.0%; Score 291; DB 15; Length 291;
Best Local Similarity 100.0%; Pred. No. 7.4e-40;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACAAAGTCGATTTAACTGTGAGAGGGTTCTGACGGGAAGACGCTGCTGCTGAACATC 60
|
Db 1 ACAAAGTCGATTTAACTGTGAGAGGGTTCTGACGGGAAGACGCTGCTGCTGAACATC 60
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QY 61 AAGTACAGAGCCAGGGGACACCTTGGGAGAGGTGGAGCTCCGCGACGACGGCTCGGAG 120
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Db 61 AAGTACAGAGCCAGGGGACACCTTGGGAGAGGTGGAGCTCCGCGACGACGGCTCGGAG 120
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QY 121 GAGTGGGAACCCATGACGAAGAAGGCGCAACCTGTCGGAGGTGAAGAGCGCAAGCCGCTC 180
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Db 121 GAGTGGGAACCCATGACGAAGAAGGCGCAACCTGTCGGAGGTGAAGAGCGCGCAAGCCGCTC 180
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QY 181 ACCGCGCCCAATGAATTCCTGCTTCTCCTCAAGGGCGGCATGAAGAAAGTCTTTCGACGAG 240
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Db 181 ACCGCGCCCAATGAATTCCTGCTTCTCCTCAAGGGCGGCATGAAGAAAGTCTTTCGACGAG 240
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QY 241 GTCATCCCGACCGCTTCAAGTGGGCAAAACCTACACCCAGATACAAT 291
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Db 241 GTCATCCCGACCGCTTCAAGTGGGCAAAACCTACACCCAGATACAAT 291
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RESULT 2
AY421969
LOCUS Phleum pratense Phl p 3 allergen gene, partial cds.
DEFINITION Phleum pratense (timothy grass)
ACCESSION AY421969
VERSION AY421969.1 GI:39841263
KEYWORDS
SOURCE
ORGANISM Phleum pratense (timothy grass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Aveneae; Phleum.

REFERENCE
AUTHORS Petersen,A., Suck,R., Cromwell,O. and Becker,W.M.
TITLE Cloning, expression and characterization of the grass pollen
allergen Phl p 3
JOURNAL Unpublished
REFERENCE
AUTHORS Petersen,A., Suck,R., Cromwell,O. and Becker,W.M.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-2003) Biochemical and Molecular Allergy,
Research Center Borstel, Parkallee 22, Borstel 23845, Germany
FEATURES
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ORIGIN
Query Match 78.0%; Score 227; DB 15; Length 294;
Best Local Similarity 89.1%; Pred. No. 5.5e-29;
Matches 245; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 13 TTAACCTGGAGAGGGTTCTGACGGGAAGACGCTGCTGCTGAACATCAAGTACACGAGG 72
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Db 16 TTTACTGTGCAGAGGGTTCCGACCCCAAGAGCTGGTCTGGAATCAAGTACACGAGG 75
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QY 73 CCAGGGGACACCTCGGAGGTGAGCTCCGCGACGCGCTCCGAGAGTGGGAACCC 132
|
Db 76 CCAGGGGACACCTCGGAGGTGAGCTCCGCGACGCGCTCCGAGAGTGGGAGGCC 135
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QY 133 ATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGGCAAGCCGCTCACCGGCCCAATG 192
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Db 136 CTGACGAAGAAGGGCAACGCTGTGGAGGTGAAGAGCTCAAGCCGCTGTTGGCCCTTC 195
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QY 193 AACTTCGCTTCTCTCCAAAGGGCGCATGAAGAACGCTTTCGACGAGGTCAATCCCCACC 252
|
Db 196 AACTTCGCTTCTATGTCACAGGGTGGCATGAGAACGCTTTCGACGAGGTCAATCCCCACC 255
|
QY 253 GCCTTCACGCTCGGCAAAACCTACACCCAGAAATA 287
|
Db 256 GCCTTCTCGATCGGCAAAACCTACAAACCGGAAGA 290
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RESULT 3
DGU25343
LOCUS Dactylis glomerata Dac gIII allergen mRNA, partial cds.
DEFINITION Dactylis glomerata Dac gIII allergen mRNA, partial cds.
ACCESSION U25343
VERSION U25343.1 GI:1825458
KEYWORDS
SOURCE
ORGANISM Dactylis glomerata (orchard grass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poaeae; Dactylis.
1 (bases 1 to 291)
Guerin-Marchand,C., Senchal,H., Bouin,A.P., Leduc-Brodard,V.,
Taudou,G., Weyer,A., Peltre,G. and David,B.
TITLE Cloning, sequencing and immunological characterization of Dac g 3,
a major allergen from Dactylis glomerata pollen
Mol. Immunol. 33 (9), 797-806 (1996)
8811075
2 (bases 1 to 291)
Guerin-Marchand,C.
Direct Submission
JOURNAL Submitted (20-APR-1995) Claudine Guerin-Marchand, Immunology,
Pasteur Institute, Docteur Roux, 28, Paris, 75724, France
LOCATION/Qualifiers
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QY 4 AAAGTCGATTTAACTGTGAGAGGGTTCTGACGGGAAGACGCTGCTGACATCAAG 63
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Db 4 AAGGTGACCTTCAAGGTGGAGAGGGTTCCGACCCCAAGAGCTGGTCTCGACATCAAG 63
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QY 64 TACACGAGCGCAGGGGACACCTTGGCGAGGTGGAGCTCCGCGACGACGCTCGGAGGAG 123
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Db 64 TACACGAGCGCAGGGGACACCTTGGCGAGGTGGAGCTCCGCGACGACGCTCGGAGGAG 123
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QY 124 TGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCAAGCCGCTCACC 183
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Db 124 TGGGAGCCCTTGAAGAGAGGGCAACCTGTGGGAGGTGAAGAGCTCCAAGCCGCTCACT 183
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QY 184 GGCCCAATGAATTCGCTTCTCCTCCAAAGGGCGCATGAAGAGCTTTCGACGAGGTC 243
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QY 244 ATCCCAACCGCTTACCGTGGCAAAACCTACACCCCA 284
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 Db 244 ATCCCAACCGCTTACCGTGGCAAAACCTACACCCCA 284
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RESULT 4

TAPOLALL
 LOCUS T.aestivum mRNA for pollen allergen-like protein. PLN 18-APR-2005
 DEFINITION Z50867
 VERSION Z50867.1 GI:972512
 KEYWORDS pollen allergen-like protein.
 SOURCE Triticum aestivum
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Balzer H.J., Borysiuk, L., Meyer, H., Matzk, F. and Baumlein, H.
 TITLE A pollen allergen encoding gene is expressed in wheat ovaries
 JOURNAL Plant J.
 REFERENCE
 AUTHORS Balzer H.J.
 TITLE Direct Submission
 JOURNAL Submitted (29-AUG-1995) Balzer H.-J., Institute of Plant Genetics
 and Crop Plant Research, Molecular Genetics, Corrensstrasse 3,
 Gatersleben, Germany, 06466

FEATURES

source

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CDS

Query Match 65.2%; Score 189.6; DB 15; Length 616;
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 Matches 225; Conservative 0;
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 Db 145 TACACAAAGGCCAAACACACAGCTGTACAGAGGTGTGAGCTCCGGCAGTACGGCTCAGAGGAG 204
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 QY 124 TGGGAACCATCAGCAAGAGGGCACCTGTGGGAGGTGAAGCGCCAGCGCTCACC 183
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 Db 205 TGGCAGCCCTTACCAAGAAGGGCGACGCTGTGGGAGGTCTCGTGTCTCAAGCGCGTGT 264
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 QY 184 GGCCCAATGAATTCGGCTTCCTCTCCAAAGGGCGGCATGAAGAACGCTCTTCGACGAGGTC 243
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ORIGIN

Query Match 65.2%; Score 189.6; DB 15; Length 616;
 Best Local Similarity 79.2%; Pred. No. 1.1e-22; Mismatches 59; Indels 0; Gaps 0;
 Matches 225; Conservative 0;
 QY 4 AAAGTCGATTTAACTGTGAGAGGGTCTTGACGGCAAGACGCTGGTGTGAACATCAAG 63
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 Db 85 AAAGTCGATTTAACTGTGAGAGGGTCTTGACGGCAAGACGCTGGTGTGAACATCAAG 144
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Db 265 GGCCCTTTCAACTTCGGCTTCTGTCCAGAAATGTCATGAAGAAAGTCTTCGACGAGGTC 324
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 QY 244 ATCCCAACCGCTTACCGTGGCAAAACCTACACCCCA 287
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 Db 325 TTCTCCACCGATTTCAGATCGGCAAAACCTACGAAACCGGAATA 368
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RESULT 5

CDAL131335 369 bp mRNA linear PLN 15-APR-2005
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 DEFINITION AJ131335
 ACCESSION AJ131335
 VERSION AJ131335.1 GI:4006977
 KEYWORDS pollen allergen (group II).
 SOURCE Cynodon dactylon (Bermuda grass)
 ORGANISM Cynodon dactylon

REFERENCE
 AUTHORS Sturaro, M. and Viotti, A.
 TITLE Isolation of cDNA from different grass species coding for
 homologues of a major pollen allergen of Phleum pratense (Phl p 2)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 369)
 AUTHORS Sturaro, M.
 TITLE Direct Submission
 JOURNAL Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
 C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
 20133, Milano, Italy

FEATURES

source

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CDS

Query Match 44.5%; Score 129.4; DB 15; Length 369;
 Best Local Similarity 70.6%; Pred. No. 2e-12; Mismatches 76; Indels 9; Gaps 2;
 Matches 204; Conservative 0;
 QY 2 CAAGAAGTCGATTTAACTGTGAGAGGGTCTTGACGGCAAGACGCTGGTGTGAACATCA 61
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 Db 83 CGAAGTGCAGTTTCAGCTGGAGAGGGGTCCACAGAGACACCTGGCGGTGCTGGA 142
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 QY 62 AGTACACAGGCCAAGGGGACACCTTGGCGGAGGTGTGAGCTCCGGCAGCAGCGCTCGGAGG 121
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 Db 143 AGTACGAG-----GGGACACCATGTGGCGAGGTGGAACTCCGGGAGCAGCGTTCGAGC 196
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 QY 122 AGTGGGAACCATGACGAA---GAAGGCAACCTCTGGGAGGTGAAGAGCGCCAGACCCG 178
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 Db 197 AGTGGGTGGCCATGAACTTCGCTTCCTCCAAAGGGGGCGGCGGTGTGACGTTCCAGACGAGGAGCCGC 256
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 QY 179 TCACCGCGCCCAATGAATTCGCTTCCTCCAAAGGGGGCGCATGAAGAACGCTTCGAGC 238
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 Db 257 TCNAGGGGCCCTTCAACTTCGGTTCCTCACCAGAGGGCGCATGAAGAACGCTTCGAGC 316
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 QY 239 AGGTCAATCCCCACCGCTTCAGCGTCGCGCAAAACCTACACCCCA 287
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Db      317 AGCTCGTCCCGGAGAGTACACCATCGGCGCCACCTACGCGCCAGAGA 365
LOCUS   LPLOLPII
DEFINITION L.perenne mRNA for allergen Lol pII.
ACCESSION X73363
VERSION   X73363.1 GI:431863
KEYWORDS allergen; ferritin; fusion protein; Lol pII; overexpression.
SOURCE    Lolium perenne
ORGANISM   Lolium perenne
REFERENCE 1 (bases 1 to 264)
AUTHORS   Sidoli,A., Tamborini,E., Giuntini,I., Levi,S., Volonte,G.,
Paini,C., De Lallia,C., Siccardi,A.G., Baralle,F.E., Galliani,S. and
Arosio,P.
TITLE     Cloning, expression, and immunological characterization of
recombinant Lolium perenne allergen Lol p II
JOURNAL   J. Biol. Chem. 268 (29), 21819-21825 (1993)
PUBMED    7691817
REFERENCE 2 (bases 1 to 264)
AUTHORS   Sidoli,A.
TITLE     Direct Submission
JOURNAL   Submitted (14-JUN-1993) A. Sidoli, Istituto Scientifico H. San
Raffaele, Dibit, Via Olgettina 58, 20132 Milano, ITALY
FEATURES             Location/Qualifiers
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Query Match      44.4%; Score 129.2; DB 15; Length 264;
Best Local Similarity 71.0%; Pred. No. 2.3e-12;
Matches 186; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY      10 GATTTAACTGTGGAGAGGTTCTGACGCGAAGACGCTGGTCTGAACATCAAGTACAG 69
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QY      70 AGCGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGCGACGACGCTCGGAGGAGTGGGAA 129
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QY      130 CCCATGACGAAGAAGGGCA-----CCTGTGGGAGGTGAAGAGCGCCAAAGCCGCTCACCGGC 186
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QY      187 CCAATGAACCTCCGCTTCTCTCCAAAGGCGCGCATGAAGACGTCTTCGACGAGGTCAATC 246
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QY      247 CCCACCGCTTCACGCTCGGCA 268
Db      241 CGCGGGACTTCAAAGTCGTA 262

RESULT 7
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LOCUS   HLAI131336
DEFINITION Holcus lanatus mRNA for pollen allergen (Hol 1 2, group II).
ACCESSION AJ131336
VERSION   AJ131336.1 GI:4007083
KEYWORDS pollen allergen (group II).

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LOCUS   DGL131334
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ACCESSION AJ131334
VERSION   AJ131334.1 GI:4007039
KEYWORDS pollen allergen (group II).
SOURCE    Dactylis glomerata
ORGANISM   Dactylis glomerata
REFERENCE 1 (bases 1 to 369)
AUTHORS   Sturaro,M. and Viotti,A.
TITLE     Isolation of cDNA from different grass species coding for
homologues of a major pollen allergen of Phleum pratense (Phl p 2)
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 369)
AUTHORS   Sturaro,M.
TITLE     Direct Submission
JOURNAL   Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
20133, Milano, Italy
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Query Match      43.4%; Score 126.2; DB 15; Length 369;
Best Local Similarity 69.9%; Pred. No. 7e-12;
Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;

QY      2 CAAGAATCGATTAACTGTGGAGAGGTTCTGACGCGAAGACGCTGCTGCTGAACATCA 61
Db      83 CGAAGGTGACGTTTACCGTGGAGAGGGGTCCAACGAGAACACCTGGCGGTGCTGGTGA 142

QY      62 AGTACACGAGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGGCAGCACCGCTCGGAGG 121
Db      143 AGTACGAG-----GGGACACCATGGCGGAGGTGGAGCTCCGGGAGCACGCTCCGAGC 196

QY      122 AGTGGGAACCATGACGAA---GAAAGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGC 178
Db      197 AGTGGGTGCGCATGACCAAGGGGGGCGCGGTGTGACGCTTCACACGAGGAGGAGCGCGC 256

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Db      257 TCCAGGGGCGCTTCAACTTCCGGTTCCTTCAACGAGAGGGGATGAAGAACGCTTTCGAGC 316

QY      239 AGGTCATCCCCCAGCCCTTTCACGGTTCGGCAAAACCTACACCCCGAATA 287
Db      317 ACGTCGTCACAGAGAGTACACCATTGGGGCCACCTACGCGCCAGAGA 365

RESULT 8
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LOCUS   HLAI131336
DEFINITION Holcus lanatus mRNA for pollen allergen (Hol 1 2, group II).
ACCESSION AJ131336
VERSION   AJ131336.1 GI:4007083
KEYWORDS pollen allergen (group II).

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SOURCE          Holcus lanatus (velvet grass)
ORGANISM        Holcus lanatus
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Pooideae; Aveneae; Holcus.
REFERENCE
AUTHORS         Sturaro, M. and Viotti, A.
TITLE           Isolation of cDNA from different grass species coding for
                homologues of a major pollen allergen of Phleum pratense (Phl p 2)
JOURNAL         Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
                20133, Milano, Italy
REFERENCE
AUTHORS         Sturaro, M.
TITLE           Direct Submission
                (bases 1 to 369)
JOURNAL         Unpublished
                2 (bases 1 to 369)
                Sturaro, M.
                Direct Submission
                Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
                20133, Milano, Italy
                C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
                20133, Milano, Italy
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Query Match      43.4%; Score 126.2; DB 15; Length 369;
Best Local Similarity 69.9%; Pred. No. 7e-12;
Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;

QY 2 CAAAGTCGATTAACTGTGGAGAGGGTTCTGACCGGAAGACGCTGGTGTGAACATCA 61
DB 83 CGAAGTGACGTTTCAAGTGGAGAGGGTCCAAACGAGAAGCACCTGGCGGTGCTGGTGA 142
QY 62 AGTACACGAGCCAGGGACACCTTGGCGGAGGTGGAGCTCCGGCAGACGCGCTCGGAGG 121
DB 143 AGTACGAG-----GGGCACACCATGGCGGAGGTGGAGCTCCGGCAGACGCGCTCGGAGG 196
QY 122 AGTGGGAACCATGACGAA---GAAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCCGC 178
DB 197 AGTGGGTGCGCATGACCAAGGGGAGGGCGGTGGACGTTTCGACGAGGAGGAGCCGC 256
QY 179 TCACCGGCCCCAATGAACCTTCGCTTCTCCAAAGGGGGCATGAAGAACGCTCTTCGAGG 238
DB 257 TCCAGGGGCCCTTCAACTTCGCTTCTCCAGGAGGCGCATGAAGAACGCTCTTCGAGG 316
QY 239 AGGTATATCCCAACCGCCCTTCACGGTCGCGCAAAACCTACACCCCGCAAGAATA 287
DB 317 ACGTGTCCAGAGAAGTACACCATTTGGGGCCACCTACGCGCCAGAGA 365

RESULT 10
LOCUS          PPRI131337
DEFINITION     Poa pratensis mRNA for pollen allergen (Poa p 2, group II).
ACCESSION      AJ131337
VERSION        AJ131337.1 GI:4007654
KEYWORDS       pollen allergen (group II).
                Poa pratensis (Kentucky bluegrass)
SOURCE         Poa pratensis
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Pooideae; Poae; Poa.
REFERENCE
AUTHORS        Sturaro, M. and Viotti, A.
TITLE          Isolation of cDNA from different grass species coding for
                homologues of a major pollen allergen of Phleum pratense (Phl p 2)
JOURNAL        Unpublished
                2 (bases 1 to 369)
                Sturaro, M.
                Direct Submission
                Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
                20133, Milano, Italy
                C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
                20133, Milano, Italy
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CDS

ORIGIN

Query Match 43.4%; Score 126.2; DB 15; Length 369;
Best Local Similarity 69.9%; Pred. No. 7e-12;
Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;
QY 2 CAAGAAGTCGATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTCTGAACATCA 61
Db 83 CGAAGGTGACGTTTACCGTGGAGAGGGTCCAAACGAGAAGCACCTGGCGGTGTGGTGA 142
QY 62 AGTACACAGAGCCAGGACACCTTGGCGAGGTGGAGTCCGGCAGACCGCTCGGAGG 121
Db 143 AGTACGAG-----GGGACACCATGCGGAGGTGGAGTCCGGGAGCACGCTCCGACG 196
QY 122 AGTGGGAACCATGACGAA---GAAGGCAACCTGTGGGAGGTGAAGAGCGCAAGCGCG 178
Db 197 AGTGGGTGCGCATGACCAAGGGGAGGGCGGTGTGGACGTTCCACAGCGAGGAGCGCGC 256
QY 179 TCACCGGCGCCCAATGAACCTTCCGCTTCTCCAAAGGGCGGCGATGAAGACGCTTTCGACG 238
Db 257 TCCAGGGGCCCTTCAACTTCCGTTCTCCACGAGAGGCGATGAAGACGCTTTCGACG 316
QY 239 AGGTGATCCCAACCGCTTACGCTGCGCAAAACCTACACCCAGCAATA 287
Db 317 AGTGTGCTCCAGAGAAGTACACCATTTGGGGCCACCTACGCGCCAGAAGA 365

RESULT 11
TAE131338
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum mRNA for pollen allergen (Tri a 2, group II).
AJ131338.1 GI:4007851
pollen allergen (group II).
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Sturaro, M. and Viotti, A.
Isolation of cDNA from different grass species coding for
homologues of a major pollen allergen of Phleum pratense (Phl p 2)
Unpublished
2 (bases 1 to 369)
Sturaro, M.
Direct Submission
Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
20133, Milano, Italy
Location/Qualifiers
1..369
/organism="Triticum aestivum"
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/note="Tri a 2"
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/product="pollen allergen (group II)"
/protein_id="CAA10349.1"
/db_xref="GI:4007852"

FEATURES

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25..393
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CDS

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ORIGIN

Query Match 43.4%; Score 126.2; DB 15; Length 369;
Best Local Similarity 69.9%; Pred. No. 7e-12;
Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;
QY 2 CAAGAAGTCGATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTCTGAACATCA 61
Db 83 CGAAGGTGACGTTTACCGTGGAGAGGGTCCAAACGAGAAGCACCTGGCGGTGTGGTGA 142
QY 62 AGTACACAGAGCCAGGACACCTTGGCGAGGTGGAGTCCGGCAGACCGCTCGGAGG 121
Db 143 AGTACGAG-----GGGACACCATGCGGAGGTGGAGTCCGGGAGCACGCTCCGACG 196
QY 122 AGTGGGAACCATGACGAA---GAAGGCAACCTGTGGGAGGTGAAGAGCGCAAGCGCG 178
Db 197 AGTGGGTGCGCATGACCAAGGGGAGGGCGGTGTGGACGTTCCACAGCGAGGAGCGCGC 256
QY 179 TCACCGGCGCCCAATGAACCTTCCGCTTCTCCAAAGGGCGGCGATGAAGACGCTTTCGACG 238
Db 257 TCCAGGGGCCCTTCAACTTCCGTTCTCCACGAGAGGCGATGAAGACGCTTTCGACG 316
QY 239 AGGTGATCCCAACCGCTTACGCTGCGCAAAACCTACACCCAGCAATA 287
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RESULT 12
PPHLP11
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
P. pratense mRNA for PHL PII pollen allergen.
X75925.1 GI:415895
allergen; PhlPII.
Phleum pratense (timothy grass)
Phleum pratense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Aveneae; Phleum.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Dolecek, C., Vrtala, S., Laffer, S., Steinberger, P., Kraft, D.,
Scheiner, O. and Valenta, R.
Molecular characterization of phl p II, a major timothy grass
(Phleum pratense) pollen allergen
FEBS Lett. 335 (3), 299-304 (1993)
8262175
2 (bases 1 to 525)
Dolecek, C.
Direct Submission
Submitted (05-NOV-1993) C. Dolecek, Ins. of General and Exp.
Pathology, General Hospital, Waehringer Guertel 18-20, 1090 Vienna,
AUSTRIA
Location/Qualifiers
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/mol_type="mRNA"
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25..393
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/db_xref="GOA:P43214"
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103..390
/product="PHL PII, pollen allergen"

FEATURES

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/mol_type="mRNA"
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ORIGIN

Query Match 43.4%; Score 126.2; DB 15; Length 525;
 Best Local Similarity 69.9%; Pred. No. 6.6e-12;
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QY 2 CAAGAAGTGAATTAAGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTGAACATCA 61
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QY 62 AGTACACGAGCGGACGCGACCCCTGGCGAGGTGGAGCTCGGCGAGCACGCTCGGAGG 121
 DB 167 AGTACGAG-----GGGACACCATGCGGAGGTGGAGCTCGGAGCACGCTCGGAGG 220

QY 122 AGTGGGAACCCATGACGAA--GAAGGGCAACCTGTGGGAGGTGAAGAGCGCAAGCGCG 178
 DB 221 AGTGGTCCCATGACCAAGGGGAGGGCGGCGTGTGGACGTTTCGACAGCGAGGAGCGC 280

QY 179 TCACCGGCGCCCAATGAATCTCGCTCTCTCAAGGGCGGCGATGAAGAACGCTTCGAGC 238
 DB 281 TCCAGGGCGCTTCAACTTCGCTTCCCTCACCGAGAGGGCATGAAGAACGCTTCGAGC 340

QY 239 AGGTATCCCAACCGCTTCAGGTCGCGCAAAACCTACACCCCAAGTA 287
 DB 341 AGCTGCTCCAGAGAAGTACACCATTTGGGGCCACCTACGCGCCAGAAGA 389

RESULT 13

LOCUS A40218 369 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 1 from Patent WO9423035.
 ACCESSION A40218
 VERSION A40218.1 GI:2296352
 KEYWORDS Phleum pratense (timothy grass)
 ORGANISM Phleum pratense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Aveneae; Phleum.
 REFERENCE 1 (bases 1 to 369)
 AUTHORS Dolecek,C., Vrtala,S., Laffer,S., Steinberger,P., Kraft,D.,
 Scheiner,O. and Valenta,R.
 TITLE RECOMBINANT TIMOTHY GRASS POLLEN ALLERGEN -I (Phl p) II
 JOURNAL Patent: WO 9423035-A 1 13-OCT-1994;
 BIOWAY PROD & HANDEL (AT)
 COMMENT Other publication CA 2136973 941013
 Other publication AU 6276894 941024
 Other publication NO 944634 950123
 Other publication FI 945648 950125
 Other publication AT 67293 960515
 Other publication JP 8500492T 960123.

FEATURES

Location/Qualifiers
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 /organism="Phleum pratense"
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 /db_xref="taxon:15957"

ORIGIN

Query Match 41.7%; Score 121.4; DB 6; Length 369;
 Best Local Similarity 68.9%; Pred. No. 4.6e-11;
 Matches 199; Conservative 0; Mismatches 81; Indels 9; Gaps 2;

QY 2 CAAGAAGTGAATTAAGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTGAACATCA 61
 DB 83 CGAAGGTGACGTTACGCTGGAGAGGGTCCACGAGAGACCTCTGGCGGTGCTGGTGA 142

QY 62 AGTACACGAGCGGACGCGACCCCTGGCGAGGTGGAGCTCGGCGAGCACGCTCGGAGG 121
 DB 143 AGTACGAG-----GGGACACCATGCGGAGGTGGAGCTCGGAGCACGCTCGGAGG 196

QY 122 AGTGGGAACCCATGACGAA--GAAGGGCAACCTGTGGGAGGTGAAGAGCGCAAGCGCG 178
 DB 197 AGTGGTCCCATGACCAAGGGGAGGGCGGCGTGTGACGCTTCGACGCTTCGACGAGGAGCGCG 256

QY 179 TCACGCGCCCAATGAATTCGCTTCTCTCAAGGGCGGCGATGAAGAACGCTTCGAGC 238
 DB 257 TCCAGGGCGCTTCAACTTCGCTTCTCTCACGAGAGGGCATGAAGAACGCTTCGAGC 316

QY 239 AGGTATCCCAACCGCTTCAGGTCGCGCAAAACCTACACCCCAAGTA 287
 DB 317 AGCTGCTCCAGAGAAGTACACCATTTGGGGCCACCTACGCGCCAGAAGA 365

RESULT 14
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 LOCUS Zea mays clone ZMMBBb0305008, *** SEQUENCING IN PROGRESS ***, 9
 DEFINITION ordered pieces.
 ACCESSION AC149815
 VERSION AC149815.2 GI:57790136
 KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 137065)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.
 and Messing,J.
 Zea mays, clone ZMMBBb0305008
 TITLE Zea mays, clone ZMMBBb0305008
 JOURNAL 2 (bases 1 to 137065)
 REFERENCE 2 (bases 1 to 137065)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.,
 Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S.,
 Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
 Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., Corum,B., DeAvellano,K., Diaz,J.S., Dodge,S.,
 Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P.,
 Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L.,
 Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P.,
 Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J.,
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylot,J., Nguyen,C.,
 Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 TITLE Zea mays, clone ZMMBBb0305008
 JOURNAL 3 (bases 1 to 137065)
 REFERENCE 3 (bases 1 to 137065)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.,
 Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S.,
 Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
 Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., Corum,B., DeAvellano,K., Diaz,J.S., Dodge,S.,
 Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P.,
 Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L.,
 Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J.,
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 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P.,
 Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J.,
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylot,J., Nguyen,C.,
 Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,

Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 14, 2005 this sequence version replaced gi:49035039.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center of MIT and Harvard
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (http://pgr.rutgers.edu)

Butler, B and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

----- Project Information
 Center project name: L30237
 Center clone name: 305_O_8

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 5214: contig of 5214 bp in length
 * 5215 5314: gap of unknown length
 * 5315 13947: contig of 8533 bp in length
 * 13948 13947: gap of unknown length
 * 13948 21146: contig of 7199 bp in length
 * 21147 21246: gap of unknown length
 * 21247 43754: contig of 22508 bp in length
 * 43755 43854: gap of unknown length
 * 43855 68442: contig of 24588 bp in length
 * 68443 68542: gap of unknown length
 * 68543 97163: contig of 28621 bp in length
 * 97164 131238: gap of unknown length
 * 131239 131338: gap of unknown length
 * 131339 135746: contig of 4408 bp in length
 * 135747 135846: gap of unknown length
 * 135847 137065: contig of 1219 bp in length.

FEATURES

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 13948..13947
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 43755..43854
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 68443..68542
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 97164..97263
 /estimated_length=unknown
 131239..131338
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gap

ORIGIN

Query Match 32.0%; Score 93; DB 14; Length 137065;
 Best Local Similarity 59.7%; Pred. No. 1.1e-06;
 Matches 175; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
 QY 2 CAAAGTCGATTTAACTGTGGAGAGGTTCTGACGCGAAGACGCTGTGTGTGAACATCA 61
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 QY 62 AGTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGCGAGCACCGCTCGGAGG 121
 DB 133628 AGTACGTCGAGCGCGATGGCGACATTTGTGGCGGTGGACATCAAGAGAGAGGCTCCGACA 133687
 QY 122 AGTGGGAACCATGACGAAGNA---GGCAACCTGTGGAGGTGAAGAGCCGACGCGC 178
 DB 133688 CGTACGAGCCCTCTAAAGCACTCTCTGGGCGCGCATCTGGAGGAAGGACAGCCGCGA 133747
 QY 179 TCACCGCGCCCAATCAACTTTCGCTTCTCTCAAGGCGCGCATGAAGAACGCTTTCGACG 238
 DB 133748 TCAAGGAGCCCATCACCCTCAACTCACCAGGAGGAGGACTTAGACCTTCTACGAG 133807
 QY 239 AGGTCAATCCCGCCCGCTTCAACGCTCGGCGCAAACTTACACCCCAAGATACAAAT 291
 DB 133808 ATGTCATCCCGCGCGCTGGAAGCCCAACACTGCTACACCGCCCAATAAACT 133860

RESULT 15

AY543539
 LOCUS AY543539 825 bp mRNA linear PLN 16-SEP-2004
 DEFINITION Triticum aestivum expansin EXPB4 mRNA, complete cds.
 ACCESSION AY543539
 VERSION AY543539.1 GI:44894801
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 825)
 AUTHORS Zhan, L., Zhong, F.N. and Qi, X.S.
 TITLE Isolation and characterization of novel expansins in wheat
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 825)
 AUTHORS Zhan, L., Zhong, F.N. and Qi, X.S.
 TITLE Direct Submission
 JOURNAL Submitted (07-FEB-2004) Plant Genetics and Breeding, China Agricultural University, Yuanmingyuan Xilu No. 2, Beijing 100094, China

FEATURES

Location/Qualifiers
 1..825
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ORIGIN

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 Matches 167; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
3629.710 Million cell updates/sec

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Perfect score: 291
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	206.2	70.9	479	5 BQ764352	BQ764352 EBan01_SQ
4	206.2	70.9	536	5 BQ764299	BQ764299 EBan01_SQ
5	206.2	70.9	554	6 CB881064	CB881064 HM08K18w
6	206.2	70.9	567	3 BM441959	BM441959 EBan01_SQ
7	206.2	70.9	571	5 BQ753338	BQ753338 EBan01_SQ
8	206.2	70.9	579	6 CB881049	CB881049 HM08J22w
9	206.2	70.9	590	3 BM442532	BM442532 EBan01_SQ
10	206.2	70.9	595	5 BU994934	BU994934 HM08K18r
11	206.2	70.9	610	3 BM442552	BM442552 EBan01_SQ
12	206.2	70.9	612	5 BU994919	BU994919 HM08J22r
13	206.2	70.9	617	3 BM442582	BM442582 EBan01_SQ
14	206.2	70.9	649	5 BQ764151	BQ764151 EBan01_SQ
15	204.6	70.3	512	3 BM442121	BM442121 EBan01_SQ
16	203	69.8	428	5 BQ753526	BQ753526 EBan01_SQ
17	203	69.8	433	5 BQ753588	BQ753588 EBan01_SQ
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19	192.8	66.3	569	3 BJ256786	BJ256786 BJ256786
20	192.8	66.3	620	3 BJ243412	BJ243412 BJ243412
21	192.8	66.3	632	3 BJ244978	BJ244978 BJ244978
22	192.8	66.3	665	3 BJ249463	BJ249463 BJ249463

23	192.8	66.3	665	3	BJ257731	BJ257731
24	192.8	66.3	673	3	BJ263153	BJ263153
25	192	66.0	646	6	CA741566	CA741566 wialc.pk0
26	191.4	65.8	429	3	BJ248460	BJ248460
27	191.4	65.8	526	3	BJ248983	BJ248983
28	191.4	65.8	534	3	BJ243229	BJ243229
29	191.4	65.8	536	6	CA595072	CA595072 wpalc.pk0
30	191.4	65.8	588	3	BJ261613	BJ261613
31	191.4	65.8	589	3	BJ249271	BJ249271
32	191.4	65.8	589	3	BJ257366	BJ257366
33	191.4	65.8	591	3	BJ246134	BJ246134
34	191.4	65.8	620	3	BJ252559	BJ252559
35	191.4	65.8	622	3	BJ256080	BJ256080
36	191.4	65.8	626	3	BJ265714	BJ265714
37	191.4	65.8	627	6	CA741405	CA741405 wialc.pk0
38	191.4	65.8	638	3	BJ259998	BJ259998
39	191.4	65.8	638	6	CA595881	CA595881 wpalc.pk0
40	191.4	65.8	646	3	BJ252576	BJ252576
41	191.4	65.8	648	3	BJ262948	BJ262948
42	191.4	65.8	655	3	BJ246668	BJ246668
43	191.4	65.8	656	3	BJ246462	BJ246462
44	191.4	65.8	656	6	CA741793	CA741793 wialc.pk0
45	191.4	65.8	657	3	BJ246639	BJ246639

ALIGNMENTS

RESULT 1
AU247615
LOCUS AU247615 FL Lolium multiflorum cDNA clone FL035B07-5, mRNA linear EST 14-MAR-2005
DEFINITION AU247615 FL Lolium multiflorum cDNA clone FL035B07-5, mRNA linear EST 14-MAR-2005
ACCESSION AU247615
VERSION AU247615.1 GI:46504884
KEYWORDS EST.
SOURCE Lolium multiflorum (Italian ryegrass)
ORGANISM Lolium multiflorum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poae; Lolium.
1 (bases 1 to 518)
Ikeda,S.
Lolium multiflorum EST Project
Unpublished (2004)
Contact: Seiji Yazaki
Japan Grassland Agriculture and Forage Seed Association
Forage Crop Research Institute (FCRI)
Higashikada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
Email: yazakis@fsas.or.jp
contact: tadashi takamizo (takamizo@affrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog.
Location/Qualifiers
1. 518
/organism="Lolium multiflorum"
/mol_type="mRNA"
/db_xref="taxon:4521"
/clone="FL035B07-5"
/tissue_type="Inflorescence"
/clone_lib="FL"

Query Match 82.6%; Score 240.4; DB 1; Length 518;
Best Local Similarity 89.3%; Pred. No. 4.9e-48;
Matches 259; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 ACAAAAGTCGATTTAACCTGGGAGAGCGTTCTACCGGAAGACGCTGCTGACATC 60
DB 21 ACGAAGTGGACCTTACCGTGGAGAGGGTCCGACGCGCAAGAGCTGGTCTTGAACATC 80

Qy	61	AAGTACACGAGGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCAGCGGCTCGGAG	120
Db	81	AAGTACACGAGTGCACGGGACACACTGGCGGAGGTCTGAGCTTCGGCAGCAGCGGCTCGGAG	140
Qy	121	GAGTGGGAA CCCATGACGAAGAGGGGCAACCTGTGGGAGGTGAAGACGCGCAAGCCGCTC	180
Db	141	GAGTGGGAGGCCATGACAAAGAGGGCAACCTGTGGGAGGTGACGAGCGCCAGCCGCTC	200
Qy	181	ACGGGCCCAATGAACCTTCGCTTCTCCAAGGGCGGCATGAAGAACGCTTTCGACGAG	240
Db	201	ACTGGCCCCAATGAACCTTCGCTTCTCCAAGGGCGGCATGAAGAACGCTTTCGACGAG	260
Qy	241	GTCATCCCCACCGCCTTCACGGTGGGCAAACTACACCCAGAAATACAA	290
Db	261	GTCATCCCCACCGCCTTCAAGATCGGACCGACCTTACACACGGAGTATAA	310

RESULT 2
 BQ764245
 LOCUS
 DEFINITION
 BQ764245 464 bp mRNA linear EST 26-JUL-2002
 Eban01_SQ005_E10_R anther, yellow stage, no treatment, cv Optic,
 Eban01_Hordeum vulgare subsp. vulgare cDNA clone Eban01_SQ005_E10
 5', mRNA sequence.
 BQ764245
 BQ764245.1 GI:21972717
 EST.
 SOURCE
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Hordeum.
 1 (bases 1 to 464)
 Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
 Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 Development of Barley Transcriptome Resources
 Unpublished (2001)
 CONTACT: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.
 Location/Qualifiers
 1..464
 FEATURES

ORIGIN	Query Match	70.9%;	Score 206.2;	DB 5;	Length 464;
	Best Local Similarity	81.8%;	Pred. No. 1e-39;		
	Matches 238;	Conservative	0;	Mismatches 53;	Indels 0;
	Gaps	0;			
Qy	1	ACAAAAGTCGATTTAACTGTGGAGAGAGGGTCTTGACGCGAAGACGCTGGTGTGTAACATC	60		
Db	105	ACGAAGGTGAAGTTTACGCTGCAGAAAGGGTTCGACGCCAAGAAGCTGGTGTGTAAGATC	164		
Qy	61	AAGTACAGAGGCCAGGGGACACCCCTGGCGGAGGTGGAGCTCCGGCAGACACGGCTCGGAG	120		

Db 165 GACTACACAGGCGACGACACCTCTCGGAGATGGAGCTCGTCAGCACGGCTCGGAG 224

Qy 121 GAGTGGGAACCCCATGACGAGAGGCGAACCTGTGGAGGTGAAGACGCGCAAGCCGCTC 180

Db 225 GAGTGGGAGCCCTTACCAAGAGGCGACGCTGTGGAGGCTGTTCGAGCTCCAAAGCCGCTC 284

Qy 181 ACCGGCCCATGAACTTCGCTTCCTCTCCAGGCGCGCATGAAGAACGTCCTTCGACGAG 240

Db 285 GTTGGGCCCCCTTCAACTTCGCTTCCTGTCCAGGGTGGCATGAAGAACGTCCTTCGACGAG 344

Qy 241 GTCATCCCCACCGCTTCACGGTCGGCAAAACCTACACCCCGAATACAAT 291

Db 345 GTCTTCTCCACCGATTTCAGATCGGCAAAACCTACGAACCCGTATATGAT 395

RESULT 3

LOCUS B0764352 479 bp mRNA linear EST 26-JUL-2002

DEFINITION EBan01_S0005_I16 R anther, yellow stage, no treatment, cv Optic, EBan01_Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ005_I16 5', mRNA sequence.

ACCESSION B0764352

VERSION B0764352.1 GI:21972824

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)

JOURNAL Contact: Waugh R, Marshall DF

COMMENT Genome Dynamics/Computational Biology Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotland, UK Tel: 00 44 1382 562731 Fax: 00 44 1382 562426 Email: est@scri.sari.ac.uk.

FEATURES

source Location/Qualifiers

1..479

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Optic"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="EBan01_SQ005_I16"

/tissue_type="anther"

/dev_stage="yellow stage"

/lab_host="DH10B"

/clone_lib="anther, yellow stage, no treatment, cv Optic, EBan01"

/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from anthers dissected from developing flowers in the glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGP (Investigating Gene Function) project."

ORIGIN

Query Match 70.9%; Score 206.2; DB 5; Length 479;

Best Local Similarity 81.8%; Pred. No. 1e-39;

Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0

Qy 1 ACAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTCTGACATC 60

Db 31 ACGAAGGTGAAGTTTCACGCGTCAGAAGGGGTCCGACGCGCAAGAAGCTGGTCTGAAGATC 90

Qy 61 AAGTACACGAGCCAGGGGACACCTCGCGAGGTGGAGTCTCCGCGAGCACCGCTCGGAG 120

ORIGIN					
	Query Match	70.9%	Score 206.2;	DB 5;	Length 479;
	Best Local Similarity	81.8%;	Pred. No. 1e-39;		
	Matches 238; Conservative	0;	Mismatches 53;	Indels	0; Gaps 0
QY	1	ACAAAAGTCGATTTAACTGTGGAGAAGGGTTC	TGCAGCGGAAGACGCTGGTGCTGAACATC	60	
Dd	31	ACGRAAGTGAAGTTCA	GCGTGCAGAAAGGGTTCGACGCCAAGAAGCTGGTGCTGAAGATC	90	
QY	61	AAGTACACAGGCCGAGGACACCTGGCGGAGTGGAGCTCCGCGACGACACGGCTCGGAG	120		

Db 91 GACTACACAAGGCGGACACCCCTCTCGGAGATGGAGCTCGGTGAGACCGCTCGGAG 150
 QY 121 GAGTGGGAACCCATGACGAGGAGGCGCAACCTGTGGGAGGTGAAGAGCCGCAAGCCGCTC 180
 Db 151 GAGTGGGAGCCCTTACCAAGAGGCGGAGCTGTGGGAGCTGTCGAGCTCCAAAGCCGCTC 210
 QY 181 ACCGGCCCAATGAATTCCTCGCTTCCTCTCCAAAGGCGGCGCATGAAGAACGCTCTTCGACGAG 240
 Db 211 GTTGGCCCCCTTCAACTTCGCTTCCTGTCCAAAGGCTGGCATGAAGAACGCTCTTCGACGAG 270
 QY 241 GTCATCCCCACCGCTTCACGCTCGGCAAAACCTACACCCAGATACAAAT 291
 Db 271 GTCTTCTCCACCGATTTCAGATFCGGCAAAACCTACGAACCCGTATATGAT 321

RESULT 4
 LOCUS BQ764299 536 bp mRNA linear EST 26-JUL-2002
 DEFINITION EBan01_SQ005_009_R anther, yellow stage, no treatment, cv Optic, EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ005_009 5', mRNA sequence.
 ACCESSION BQ764299
 VERSION BQ764299.1 GI:21972771
 SOURCE EST.
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 536)
 AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 JOURNAL Development of Barley Transcriptome Resources
 COMMENT Unpublished (2001)
 CONTACT: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.
 FEATURES
 source
 location/Qualifiers
 1..536
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="EBan01_SQ005_009"
 /tissue_type="anther"
 /dev_stage="yellow stage"
 /lab_host="DH10B"
 /clone_lib="anther, yellow stage, no treatment, cv Optic, EBan01"
 /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from anthers dissected from developing flowers in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

ORIGIN
 Query Match 70.9%; Score 206.2; DB 5; Length 536;
 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 1 ACAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATC 60
 Db 98 ACGAGGTGAAGTTACGGTGCAGAGAGGGTTCGACGCGCAAGAGCTGGTGTGAAGATC 157
 QY 61 AAGTACACGAGCCAGGGGACACCTTCGCGGAGGTGGAGCTCCGCGACACCGCTCGGAG 120
 Db 158 GACTACACAAGGCGGACACCCCTCTCGGAGATGGAGTCCGTGAGCAGCAGCGCTCGGAG 217

QY 121 GAGTGGGAACCCATGACGAGGAGGCGCAACCTGTGGGAGGTGAAGAGCCGCAAGCCGCTC 180
 Db 218 GAGTGGGAGCCCTTACCAAGAGGCGGAGCTGTGGGAGCTGTCGAGCTCCAAAGCCGCTC 277
 QY 181 ACCGGCCCAATGAATTCCTCGCTTCCTCTCCAAAGGCGGCGCATGAAGAACGCTCTTCGACGAG 240
 Db 278 GTTGGCCCCCTTCAACTTCGCTTCCTGTCCAAAGGCTGGCATGAAGAACGCTCTTCGACGAG 337
 QY 241 GTCATCCCCACCGCTTCACGCTCGGCAAAACCTACACCCAGATACAAAT 291
 Db 338 GTCTTCTCCACCGATTTCAGATCGGCAAAACCTACGAACCCGTATATGAT 388

RESULT 5
 LOCUS CB881064/c 554 bp mRNA linear EST 23-APR-2003
 DEFINITION HM08K18w HM Hordeum vulgare subsp. vulgare cDNA clone HM08K18 3-PRIME, mRNA sequence.
 ACCESSION CB881064
 VERSION CB881064.1 GI:30083056
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 554)
 AUTHORS Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
 JOURNAL EST sequencing and analysis in barley (2002)
 COMMENT Unpublished (2002)
 CONTACT: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 554 Std Error: 0.00
 Plate: 8 Row: K Column: 18
 Seq primer: T7.
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 location/Qualifiers
 1..554
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Barke"
 /sub_species="vulgare"
 /db_xref="GABI:559610"
 /db_xref="taxon:112509"
 /clone="HM08K18"
 /tissue_type="male inflorescences"
 /dev_stage="male inflorescences (approx. 2 mm in size), green anther stage"
 /lab_host="XL10-Gold"
 /clone_lib="HM"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN
 Query Match 70.9%; Score 206.2; DB 6; Length 554;
 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 1 ACAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATC 60
 Db 522 ACGAAGGTGAAGTTACCGTGCAGAGGGGTTCGACGCGCAAGAGCTGGTGTGAAGATC 463


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QY      61  AAGTACACAGGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAG 120
DB      151  GACTACACAAGGCGAGCGACACCTCTCGGAGATGGAGCTCCGTGAGCAGCGCTCGGAG 210
QY      121  GAGTGGGAAACCATGACGAGGAAGGCAACCTTGGGAGGTGAAGAGCCCAAGCCGCTC 180
DB      211  GAGTGGGAGCCCTTCAACCAAGGAGGCGGAGCTGTGGGAGCTGTGAGCTCCAAGCCGCTC 270
QY      181  ACCGGGCCCAATGAATTCCTCCCTTCTCCAGGGCGGCATGAAGAACTGTTTCGACGAG 240
DB      271  GTTGGCCCTTCACTTCGCTTCTGTCAGGGTGGCATGAAGAACTGTTTCGACGAG 330
QY      241  GTCATCCCAACCGCTTCAAGTTCGCTCGCAAAACCTACACCCCAAGAACTATCAAT 291
DB      331  GTCTTCTCCACCGATTCAAGATCGGCAAAACCTACGAAACCGGTATATGAT 381

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RESULT 8
CB881049/c
LOCUS   HM08J22w HM Hordeum vulgare subsp. vulgare cDNA clone HM08J22
DEFINITION
3-PRIME, mRNA sequence.

```

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ACCESSION   CB881049
VERSION     CB881049.1
KEYWORDS    GI:30083041
SOURCE      Hordeum vulgare subsp. vulgare

```

```

ORGANISM    Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

```

```

REFERENCE   1 (bases 1 to 579)
AUTHORS    Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
TITLE      EST sequencing and analysis in barley (2002)
JOURNAL    Unpublished (2002)

```

```

COMMENT     Contact: Stein Nils
            Molecular Markers Group, Department Genbank
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Corrensstr. 3, 06466, Gatersleben, Germany

```

```

Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 579 Std Error: 0.00
Plate: 8 row: J column: 22
Seq primer: T7.

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FEATURES             Location/Qualifiers
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                     /organism="Hordeum vulgare subsp. vulgare"
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                     /cultivar="Barke"
                     /sub_species="vulgare"
                     /db_xref="GABI:559595"
                     /db_xref="taxon:112509"
                     /clone="HM08J22"
                     /tissue_type="male inflorescences"
                     /dev_stage="male inflorescences (approx. 2 mm in size),
green anther stage"
                     /lab_host="XL10-Gold"
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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

```

ORIGIN

```

Query Match      70.9%; Score 206.2; DB 6; Length 579;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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QY      1  ACAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGCTGTGAACATC 60
DB      522  ACGAAGGTGAAGTTACGGGTGAGAAGGGGTCCGACCGCCAGAAAGTGTGCTGAAGATC 463
QY      61  AAGTACACGAGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAG 120
DB      462  GACTACACAAGGCGAGCGACACCTCTCGGAGATGGAGCTCCGTGAGCAGCGCTCGGAG 403
QY      121  GAGTGGGAAACCATGACGAGGAAGGCAACCTTGGGAGGTGAAGAACTGTTTCGACGAG 180
DB      402  GAGTGGGAGCCCTTCAACCAAGGAGGCGGAGCTGTGGGAGCTGTGAGCTTCAAGCCGCTC 343
QY      181  ACCGGGCCCAATGAATTCCTCCCTTCTCCAGGGCGGCATGAAGAACTGTTTCGACGAG 240
DB      342  GTTGGCCCTTCACTTCGCTTCTGTCAGGGTGGCATGAAGAACTGTTTCGACGAG 283
QY      241  GTCATCCCAACCGCTTCAAGTTCGCTCGCAAAACCTACACCCCAAGAACTATCAAT 291
DB      282  GTCTTCTCCACCGATTCAAGATCGGCAAAACCTACGAAACCGGTATATGAT 232

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RESULT 9
BM442532
LOCUS   BM442532
DEFINITION

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```

590 bp mRNA linear EST 23-JUL-2002
EBan01 SQ003_H04_R anther, yellow stage, no treatment, cv Optic,
EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ003_H04
5', mRNA sequence.

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```

ACCESSION   BM442532
VERSION     BM442532.2
KEYWORDS    GI:21931612
SOURCE      Hordeum vulgare subsp. vulgare

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```

ORGANISM    Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

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REFERENCE   1 (bases 1 to 590)
AUTHORS    Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
            Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.

```

```

TITLE      Development of Barley Transcriptome Resources
JOURNAL    Unpublished (2001)

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COMMENT     On Feb 1, 2002 this sequence version replaced gi:18473307.
            Contact: Waugh R, Marshall DP
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk
            All sequence has a Phred quality score of 20 or over
            Seq primer: M13 reverse.

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FEATURES             Location/Qualifiers
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                     /organism="Hordeum vulgare subsp. vulgare"
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                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="EBan01_SQ003_H04"
                     /tissue_type="anther"
                     /dev_stage="yellow stage"
                     /lab_host="DH10B"
                     /clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"

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/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in the
glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SEERAD funded
cereal IGF (Investigating Gene Function) project."

```

ORIGIN

```

Query Match      70.9%; Score 206.2; DB 3; Length 590;
Best Local Similarity 81.8%; Pred. No. 1e-39;

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Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGGGAAGACGCTGGTCTGAACATC 60
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 Db 99 ACGAAGGTGAAGTTTACCGGTGCAGAGGGGTGGACGCCAAGAGCTGGTCTGAAGATC 158
 |||||
 Qy 61 AAGTACACAGGAGCCAGGAGGACACCTCTGGCGAGGTGGAGCTCCGGCAGCAGCGCTCGGAG 120
 |||||
 Db 159 GACTACACAAGGAGGAGGACACCTCTCGGAGATGGAGCTCCGTGACAGCGGCTCGGAG 218
 |||||
 Qy 121 GAGTGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCTC 180
 |||||
 Db 219 GAGTGGGAGCCCTTCAACAAGAAGGGCGACGTGTGGAGCTGTGAGCTTCAAGCCGCTC 278
 |||||
 Qy 181 ACCGGCCCAATGAATCTCGCTTCTCTCCAAAGGGCGCATGAAGAACTCTTCGACGAG 240
 |||||
 Db 279 GTTGGCCCTTCAACTTCGCTTCTGTCCAAAGGGTGGCATGAAGAACTCTTCGACGAG 338
 |||||
 Qy 241 GTCATCCCCACCGCTTCAAGTCCGGCAAAACCTACACCCAGAAATACAAT 291
 |||||
 Db 339 GTCTTCTCACCGATTTCAAGATCGGCAAAACCTACGAAACCGTATATGAT 389
 |||||

RESULT 10
 BU994934
 LOCUS HM08K18r HM Hordeum vulgare subsp. vulgare cDNA clone HM08K18
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BU994934
 VERSION BU994934.1 GI:24271917
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 595)
 Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
 EST sequencing and analysis in barley (2002)
 Unpublished (2002)
 Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 595 Std Error: 0.00
 Plate: 8 row: K column: 18
 Seq primer: M13rev.
 Location/Qualifiers
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 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Barke"
 /sub_species="vulgare"
 /db_xref="GABI:254755"
 /db_xref="taxon:112509"
 /clone="HM08K18"
 /tissue_type="male inflorescences"
 /dev_stage="male inflorescences (approx. 2 mm in size),
 green anther stage"
 /lab_host="Xl10-Gold"
 /clone_lib="HM"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable."

FEATURES source

1..595
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Barke"
 /sub_species="vulgare"
 /db_xref="GABI:254755"
 /db_xref="taxon:112509"
 /clone="HM08K18"
 /tissue_type="male inflorescences"
 /dev_stage="male inflorescences (approx. 2 mm in size),
 green anther stage"
 /lab_host="Xl10-Gold"
 /clone_lib="HM"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable."

ORIGIN

Query Match 70.9%; Score 206.2; DB 5; Length 595;
 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGGGAAGACGCTGGTCTGAACATC 60
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 Db 96 ACGAAGGTGAAGTTTACCGGTGCAGAGGGGTGGACGCCAAGAGCTGGTCTGAAGATC 155
 |||||
 Qy 61 AAGTACACAGGAGCCAGGAGGACACCTCTGGCGAGGTGGAGCTCCGGCAGCAGCGCTCGGAG 120
 |||||
 Db 156 GACTACACAAGGAGGAGGAGCACCCTCTCGGAGATGGAGCTCCGTGACAGCGGCTCGGAG 215
 |||||
 Qy 121 GAGTGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCTC 180
 |||||
 Db 216 GAGTGGGAGCCCTTCAACAAGAAGGGCGACGTGTGGGAGCTGTGAGCTTCAAGCCGCTC 275
 |||||
 Qy 181 ACCGGCCCAATGAATCTCGCTTCTCTCCAAAGGGCGCATGAAGAACTCTTCGACGAG 240
 |||||
 Db 276 GTTGGCCCTTCAACTTCGCTTCTGTCCAAAGGGTGGCATGAAGAACTCTTCGACGAG 335
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 Qy 241 GTCATCCCCACCGCTTCAAGTCCGGCAAAACCTACACCCAGAAATACAAT 291
 |||||
 Db 336 GTCTTCTCACCGATTTCAAGATCGGCAAAACCTACGAAACCGTATATGAT 386
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RESULT 11
 BM442552
 LOCUS BM442552
 DEFINITION BM442552 610 bp mRNA linear EST 23-JUL-2002
 EBan01 SQ003_I01_R anther, yellow stage, no treatment, cv Optic,
 EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ003_I01
 5', mRNA sequence.
 ACCESSION BM442552
 VERSION BM442552.2 GI:21931632
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 610)
 Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
 Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
 Development of Barley Transcriptome Resources
 Unpublished (2001)
 On Feb 1, 2002 this sequence version replaced gi:18473327.
 Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk
 All sequence has a Phred quality score of 20 or over
 Seq primer: M13 reverse.

FEATURES Location/Qualifiers

1..610
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
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 /tissue_type="anther"
 /dev_stage="yellow stage"
 /lab_host="DH10B"
 /clone_lib="anther, yellow stage, no treatment, cv Optic,
 EBan01"
 /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
 Non-normalised library, directionally cloned into pSPORT1.
 Derived from anthers dissected from developing flowers in
 the glasshouse grown barley plants. Developed as part of the
 barley transcriptome resources of BBSRC/SEERAD funded

cereal IGF (Investigating Gene Function) project."

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ORIGIN
Query Match      70.9%; Score 206.2; DB 3; Length 610;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTAACTGTGAGAAAGGGTTCTGACCGCAAGACGCTGTGTCTGAACATC 60
DB 110 ACGAAGGTGAAGTTACCGGTGCAGAAAGGGTCCGACGCCCAAGAAAGCTGTGTCTGAAGATC 169

QY 61 AAGTACACGAGCCGAGGACACCTTGGCGGAGGTGAGCTCCGACGACCGCTCGGAG 120
DB 170 GACTACACAAGGCGAGGACACCTTCTCGGAGATGGAGCTCCGTGAGCAGCGCTCGGAG 229

QY 121 GAGTGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCCCAAGCGCTC 180
DB 230 GAGTGGGAGCCCTTCAACCAAGAAGGGGACGCTGTGGGAGCTGTGAGCTTCAAGCGCTC 289

QY 181 ACCGGCCCAATGAATCTTCGCTTCTCTCCAAAGGGCGGCATGAAGAAGCTTTCGACGAG 240
DB 290 GTTGGCCCCCTTCAACTTCGCTTCTCTCCAAAGGGTGGCATGAAGAAGCTTTCGACGAG 349

QY 241 GTCATCCCCACCGCTTCAAGGTCGCAAAACCTACACCCCAAGATACAT 291
DB 350 GTCCTTCTCCACCGATTTCAAGATCGCAAAACCTACGACCGGTATATGAT 400

RESULT 12
BU994919
LOCUS HM08J22r HM Hordeum vulgare subsp. vulgare cDNA clone HM08J22
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BU994919
VERSION BU994919.1 GI:24271902
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 612)
Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 612 Std Error: 0.00
Plate: 8 row: J column: 22
Seq primer: M13rev.
Location/Qualifiers
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/db_xref="GABI:254740"
/db_xref="taxon:112509"
/clone="HM08J22"
/tissue_type="male inflorescences"
/dev_stage="male inflorescences (approx. 2 mm in size),
green anther stage"
/lab_host="XL10-Gold"
/clone_lib="HM"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for

cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sali, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

ORIGIN
Query Match      70.9%; Score 206.2; DB 5; Length 612;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTAACTGTGAGAAAGGGTTCTGACCGCAAGACGCTGTGTCTGAACATC 60
DB 95 ACGAAGGTGAAGTTACCGGTGCAGAAAGGGTCCGACGCCCAAGAAAGCTGTGTCTGAAGATC 154

QY 61 AAGTACACGAGCCGAGGACACCTTGGCGGAGGTGAGCTCCGACGACCGCTCGGAG 120
DB 155 GACTACACAAGGCGAGGACACCTTCTCGGAGATGGAGCTCCGTGAGCAGCGCTCGGAG 214

QY 121 GAGTGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGCCCAAGCGCTC 180
DB 215 GAGTGGGAGCCCTTCAACCAAGAAGGGGACGCTGTGGGAGCTGTGAGCTTCAAGCGCTC 274

QY 181 ACCGGCCCAATGAATCTTCGCTTCTCTCCAAAGGGCGGCATGAAGAAGCTTTCGACGAG 240
DB 275 GTTGGCCCCCTTCAACTTCGCTTCTCTCCAAAGGGTGGCATGAAGAAGCTTTCGACGAG 334

QY 241 GTCATCCCCACCGCTTCAAGGTCGCAAAACCTACACCCCAAGATACAT 291
DB 335 GTCCTTCTCCACCGATTTCAAGATCGCAAAACCTACGACCGGTATATGAT 385

RESULT 13
BM442582
LOCUS EBan01 SQ003 J10 R anther, yellow stage, no treatment, cv Optic,
DEFINITION 5', mRNA sequence.
ACCESSION BM442582
VERSION BM442582.2 GI:21931660
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 617)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Feb 1, 2002 this sequence version replaced gi:18473357.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1. 617
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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/sub_species="vulgare"
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/clone="EBan01_SQ003_J10"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"
FEATURES
source

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/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in
glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SEERAD funded
cereal IGF (Investigating Gene Function) project."

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ORIGIN
Query Match      70.9%; Score 206.2; DB 3; Length 617;
Best Local Similarity 81.8%; Pred. No. 1e-39; Indels 0; Gaps 0;
Matches 238; Conservative 0; Mismatches 53;

QY 1 ACAAAGTCGATTAACTGTGGAGAGGGTTCTGACCGAAGACGGTGTGCTGAACATC 60
   |||
Db 98 ACAGAGGTGAAGTTACCGGTGCGAGAGGGTTCGACGCCCAAGAGCTGGTGAAGATC 157
   |||

QY 61 AAGTACACGAGGCGCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGTCCGGAG 120
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Db 158 GACTACACAGGGCAGCGGACACCTCTCGAGATGAGCTCCGTCAGCAGCGGCTCGGAG 217
   |||

QY 121 GAGTGGAAACCCATGACAGAGAGGGCAACCTGTGGAGGTGAAGAGCGGCCAGCCGCTC 180
   |||
Db 218 GAGTGGAGGCGCTTCACCAAGAGGGGACGTTGGGAGGTGTCGAGCTCCAGCCGCTC 277
   |||

QY 181 ACCGGCCCATGACTTCCGCTTCTCTCAAGGGCGGCATGAAGAACGCTTTCGACGAG 240
   |||
Db 278 GTTGGCCCTTCACACTTCCGCTTCTCTCAAGGGTGGCATGAAGAGCTTTCGACGAG 337
   |||

QY 241 GTCATCCCGCCGCTTCACCGTTCGGCAAAACCTACACCCCGAATCAAT 291
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Db 338 GTCCTTCCCGGATTCAGATCGGCAGAACCTACGAACCCGTATATGAT 388
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RESULT 14
LOCUS      BQ764151
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5', mRNA sequence.
ACCESSION  BQ764151
VERSION    BQ764151.1 GI:21972623
KEYWORDS   EST
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
REFERENCE  1 (bases 1 to 649)
AUTHORS    Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE      Development of Barley Transcriptome Resources
JOURNAL    Unpublished (2001)
COMMENT    Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
Location/Qualifiers
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/sub_species="vulgare"
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/clone="EBan01_SQ005_B03"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
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/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;

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FEATURES
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/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBan01_SQ005_B03"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;

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Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in
glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SEERAD funded
cereal IGF (Investigating Gene Function) project."

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ORIGIN
Query Match      70.9%; Score 206.2; DB 5; Length 649;
Best Local Similarity 81.8%; Pred. No. 1.1e-39; Indels 0; Gaps 0;
Matches 238; Conservative 0; Mismatches 53;

QY 1 ACAAAGTCGATTAACTGTGGAGAGGGTTCTGACCGAAGACGGTGTGCTGAACATC 60
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Db 137 ACAGAGGTGAAGTTACCGGTGCGAGAGGGTTCGACGCCCAAGAGCTGGTGAAGATC 196
   |||

QY 61 AAGTACACGAGGCGCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGTCCGGAG 120
   |||
Db 197 GACTACACAGGGCAGCGGACACCTCTCGAGATGAGCTCCGTCAGCAGCGGCTCGGAG 256
   |||

QY 121 GAGTGGAAACCCATGACAGAGAGGGCAACCTGTGGAGGTGAAGAGCGGCCAGCCGCTC 180
   |||
Db 257 GAGTGGAGGCGCTTCACCAAGAGGGGACGTTGGGAGGTGTCGAGCTCCAGCCGCTC 316
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QY 181 ACCGGCCCATGACTTCCGCTTCTCTCAAGGGCGGCATGAAGAACGCTTTCGACGAG 240
   |||
Db 317 GTTGGCCCTTCACACTTCCGCTTCTCTCAAGGGTGGCATGAAGAACGCTTTCGACGAG 376
   |||

QY 241 GTCATCCCGCCGCTTCACCGTTCGGCAAAACCTACACCCCGAATCAAT 291
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Db 377 GTCCTTCCCGGATTCAGATCGGCAGAACCTACGAACCCGTATATGAT 427
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RESULT 15
LOCUS      BM442121
DEFINITION EBan01_SQ002_E10_R anther, yellow stage, no treatment, cv Optic,
5', mRNA sequence.
ACCESSION  BM442121
VERSION    BM442121.2 GI:21931214
KEYWORDS   EST
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
REFERENCE  1 (bases 1 to 512)
AUTHORS    Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE      Development of Barley Transcriptome Resources
JOURNAL    Unpublished (2001)
COMMENT    Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1. .512
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/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
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FEATURES
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/clone="EBan01_SQ002_E10"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
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EBan01"

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:40 ; Search time 243.744 Seconds
(without alignments)
280.771 Million cell updates/sec

Title: US-10-628-296A-2
Perfect score: 513
Sequence: 1 TKVDLTVEKGSDAKTLVLNI.....FDEVIPTFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	100.0	97	1 MPAL3_LOLPR	P14948 lolium pere
2	513	100.0	97	2 Q540P9_LOLPR	Q540P9 lolium pere
3	433	84.4	96	1 MPAG3_DACGL	P93124 dactylis gl
4	422	82.3	97	2 Q69B42_PHLPR	Q69B42 phleum prat
5	366	71.3	118	2 Q41576_WHEAT	Q41576 triticum ae
6	312.5	60.9	97	1 MPAL2_LOLPR	P14947 lolium pere
7	292.5	57.0	122	1 MPAP2_PHLPR	P43214 phleum prat
8	292.5	57.0	122	2 Q712N1_9POL	Q712N1 lolium ital
9	292.5	57.0	122	2 Q712N2_WHEAT	Q712N2 triticum ae
10	292.5	57.0	122	2 Q712N3_POAPR	Q712N3 poa pratens
11	292.5	57.0	122	2 Q712N4_HOLLA	Q712N4 holcus lana
12	292.5	57.0	122	2 Q92RU0_CYNDA	Q92RU0 cynodon dac
13	292.5	57.0	122	2 Q92RU1_DACGL	Q92RU1 dactylis gl
14	281.5	54.9	88	2 Q40239_LOLPR	Q40239 lolium pere
15	167.5	32.7	267	2 Q8H7T4_ORYSA	Q8H7T4 oryza sativ
16	167.5	32.7	267	2 Q9LD05_ORYSA	Q9LD05 oryza sativ
17	166.5	32.5	267	2 Q8GSC5_ORYSA	Q8GSC5 oryza sativ
18	166.5	32.5	267	2 Q946J4_ORYSA	Q946J4 oryza sativ
19	166.5	32.5	267	2 Q9LD01_ORYSA	Q9LD01 oryza sativ
20	165	32.2	117	2 Q67W98_ORYSA	Q67W98 oryza sativ
21	164	32.0	117	2 Q7XVQ4_ORYSA	Q7XVQ4 oryza sativ
22	163	31.8	117	2 Q7XVQ2_ORYSA	Q7XVQ2 oryza sativ
23	163	31.8	117	2 Q7XVQ3_ORYSA	Q7XVQ3 oryza sativ
24	162	31.6	117	2 Q7X7H1_ORYSA	Q7X7H1 oryza sativ
25	162	31.6	117	2 Q7X1W2_ORYSA	Q7X1W2 oryza sativ
26	159	31.0	113	2 Q654A7_ORYSA	Q654A7 oryza sativ
27	157	30.6	117	2 Q653Z7_ORYSA	Q653Z7 oryza sativ
28	157	30.6	117	2 Q654A4_ORYSA	Q654A4 oryza sativ
29	157	30.6	117	2 Q654A6_ORYSA	Q654A6 oryza sativ
30	156	30.4	117	2 Q654A8_ORYSA	Q654A8 oryza sativ
31	155.5	30.3	263	2 Q9ZP03_POAPR	Q9ZP03 poa pratens

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33	152.5	29.7	263	1 MPAC1_ORYSA	Q40638 oryza sativ
34	151	29.4	118	2 Q654B1_ORYSA	Q654B1 oryza sativ
35	150.5	29.3	264	2 Q7XAX7_DACGL	Q7XAX7 dactylis gl
36	150.5	29.3	270	2 Q6QFA0_WHEAT	Q6QFA0 triticum ae
37	149.5	29.1	263	1 MPAP1_PHLPR	P43213 phleum prat
38	147.5	28.8	240	2 Q7XAX8_DACGL	Q7XAX8 dactylis gl
39	146	28.5	112	2 Q7XYF2_CYNDA	Q7XYF2 cynodon dac
40	145.5	28.4	102	2 Q6QN90_WHEAT	Q6QN90 triticum ae
41	145.5	28.4	265	2 Q6QN87_WHEAT	Q6QN87 triticum ae
42	143.5	28.0	263	2 Q9ZP13_HOLLA	Q9ZP13 holcus lana
43	143.5	28.0	265	2 Q6QF99_WHEAT	Q6QF99 triticum ae
44	143	27.9	118	2 Q654B2_ORYSA	Q654B2 oryza sativ
45	142.5	27.8	263	1 MPAL1_LOLPR	P14946 lolium pere

ALIGNMENTS

RESULT 1
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ID MPAL3_LOLPR STANDARD; PRT; 97 AA.
AC P14948;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Pollen allergen Lol p 3 (Lol p III).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90105394; PubMed=2605214;
RA Ansari A.A.; Shenbagamurthi P.; Marsh D.G.;
RT "Complete primary structure of a Lolium perenne (perennial rye grass)
pollen allergen, Lol p III: comparison with known Lol p I and II
sequences.";
RL Biochemistry 28:8665-8670(1989).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
pollen allergy. Binds to IgE.
CC -!- SIMILARITY: Belongs to the expansin family.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC PIR; A33422; A33422.
CC HSP; P43214; LWHO.
CC Gramene; P14948; .
CC InterPro; IPR005453; Allergen Lolp2.
CC InterPro; IPR007117; Expan_Lol_pI_C.
CC Pfam; PF01357; Pollen_allerg_1; 1.
CC PRINTS; PR01637; LOLP2ALLERGN.
CC PROSITE; PS50843; EXPANSIN_CBD; 1.
KW Allergen; Direct protein sequencing; Multigene family.
FT DOMAIN 14 94
FT VARIANT 6 6 T -> M.
SQ SEQUENCE 97 AA; 10907 MW; ABBAEDE2D6F20D24 CRC64;

Query Match 100.0%; Score 513; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e-48;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEWEPEMTKKNLWEVKSAPL 60
DB 1 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEWEPEMTKKNLWEVKSAPL 60

AC Q41576;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
 DE Pollen allergen-like protein.
 GN Name=Tri a III;
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=var. Salmon; TISSUE=Gynoecia;
 RA Balzer H.J.;
 RA Balzer H.J., Borysiuk L., Meyer H., Matz F., Baumlein H.;
 RT "A pollen allergen encoding gene is expressed in wheat ovaries";
 RL Plant J. 0:0-0(0).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=var. Salmon; TISSUE=Gynoecia;
 RA Balzer H.J.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z50867; CAA90746.1; -; mRNA.
 DR PIR; T06550; T06550.
 DR HSSP; P43214; IWHO.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR InterPro; IPR005453; Allergen Lolp2.
 DR InterPro; IPR007117; Expan_Lol_pI_C.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01637; Lolp2ALLERGN.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 SQ SEQUENCE 118 AA; 13262 MW; 76EA78BA219A8587 CRC64;

Query Match 71.3%; Score 366; DB 2; Length 118;
 Best Local Similarity 70.5%; Pred. No. 4.9e-32;
 Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 2 KVDLTVEKSGDAKTLVNIKTRPGDTLAEVLRQHGSEEWEPMTKGNLMEVKSAPLIT 61
 DB 24 KVLTVQKSGDKKLLALIDYTRPNDLSLSEVELRQYGSSEWQPLTKGVDVWVSCSKPLV 83

OY 62 GPMNFRFLSKGMKGVFDEVIPTAFTVGKTYTPEY 96
 DB 84 GPFNFRFLSKGMKGVFDEVFSTDFKIGKTYRPEY 118

RESULT 6
 ID MPAL2_LOLPR STANDARD; PRT; 97 AA.
 AC P14947;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Pollen allergen Lol p 2-A (lol p II-A).
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Poaceae; Lolium.
 OX NCBI_TaxID=4522;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Ansari A.A., Shenbagamurthi P., Marsh D.G.;
 RT "Complete amino acid sequence of a Lolium perenne (perennial rye grass) pollen allergen, Lol p II.";
 RL J. Biol. Chem. 264:11181-11185(1989).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass pollen allergy. Binds to IgE.
 CC -!- SIMILARITY: Belongs to the expansin family.
 CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR PIR; A34291; A34291.
 DR HSSP; P43214; IWHO.
 DR Gramene; P14947; -.
 DR InterPro; IPR005453; Allergen Lolp2.
 DR InterPro; IPR007117; Expan_Lol_pI_C.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01637; Lolp2ALLERGN.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 KW Allergen; Direct protein sequencing; Multigene family.
 FT DOMAIN 15 96 Expansin-like CBD.
 FT VARIANT 29 29 S -> A.
 FT VARIANT 49 49 N -> D.
 FT VARIANT 59 59 D -> E.
 FT VARIANT 76 76 M -> E.
 SQ SEQUENCE 97 AA; 10880 MW; 91A7DDB5DEA5BDD7 CRC64;

Query Match 60.9%; Score 312.5; DB 1; Length 97;
 Best Local Similarity 60.6%; Pred. No. 2.9e-26;
 Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

OY 3 VDLTVEKSGDAKTLVNIKTRPGDTLAEVLRQHGSEEWEPMTKGN-LMEVKSAPLIT 61
 DB 4 VFTVEKSGDEKLNLSIKYNKEGDSMAEVELKEHSGNEWLALKNGDGVWEIKSKDKPLK 63

OY 62 GPMNFRFLSKGMKGVFDEVIPTAFTVGKTYTPEY 95
 DB 64 GPFNFRFLSKGMKGVFDDVVPADPKVGTYYKPE 97

RESULT 7
 ID MPAP2_PHLPR STANDARD; PRT; 122 AA.
 AC P43214;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Pollen allergen Phl p 2 precursor (Phl p II).
 GN Name=PHLPII;
 OS Phleum pratense (Common timothy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Aveneae; Phleum.
 OX NCBI_TaxID=15957;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=94085541; PubMed=8262175; DOI=10.1016/0014-5793(93)80406-K;
 RA Dolecek C., Vrtala S., Laffer S., Steinberger P., Kraft D.,
 RA Scheiner O., Valenta R.;
 RT "Molecular characterization of Phl p II, a major timothy grass (Phleum pratense) pollen allergen.";
 RL FEBS Lett. 335:299-304(1993).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97276803; PubMed=9130496;
 RA Fedorov A.A., Ball T., Valenta R., Almo S.C.;
 RT "X-ray crystal structures of birch pollen profilin and Phl p 2.";
 RL Int. Arch. Allergy Immunol. 113:109-113(1997).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99404940; PubMed=10467147; DOI=10.1016/S0969-2126(99)80121-X;
 RA De Marino S., Morelli M.A.C., Fraternali F., Tamborini E., Musco G.,
 RA Vrtala S., Dolecek C., Arosio P., Valenta R., Pastore A.;
 RT "An immunoglobulin-like fold in a major plant allergen: the solution structure of Phl p 2 from timothy grass pollen.";
 RL Structure 7:943-952(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Pollen specific.

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CC CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
CC CC pollen allergy. Binds to IgE.
CC CC -!- SIMILARITY: Belongs to the expansin family.
CC CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC DR EMBL; X75925; CAA53529.1; -; mRNA.
CC DR PIR; S39457; S39457.
CC DR PDB; 1HWI; NMR; @=27-122.
CC DR PDB; 1WHP; X-ray; @=27-122.
CC DR PDB; 1WHP; X-ray; @=27-122.
CC DR InterPro; IPR005453; Allergen_Lolp2.
CC DR InterPro; IPR007117; Expan_Lol_pi_C.
CC DR Pfam; PF01357; Pollen_allerg_1; 1.
CC DR PRINTS; PR01637; L0LP2ALLERGN.
CC DR PROSITE; PS50843; EXPANSIN_CBD; 1.
CC DR 3D-structure; Allergen; Multigene family; Signal.
CC KW SIGNAL 1
CC FT CHAIN 27 122
CC FT DOMAIN 41 120
CC FT STRAND 30 34
CC FT TURN 36 37
CC FT STRAND 39 39
CC FT TURN 40 41
CC FT STRAND 42 49
CC FT TURN 50 51
CC FT STRAND 54 60
CC FT TURN 62 63
CC FT STRAND 68 69
CC FT STRAND 71 72
CC FT TURN 75 76
CC FT STRAND 77 81
CC FT TURN 90 96
CC FT STRAND 97 98
CC FT STRAND 101 108
CC FT TURN 114 115
CC FT STRAND 117 118
CC SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 1; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKYPDGLTAEVLRHSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTMAEVELRHGSDWEVAMTKGEGVWTFDSEPL 86

QY 61 TGPNNFRFLSKGMKNVDFEVIPTAFTVGKTYTPE 95
DB 87 QGPFNFRFLTEKGMKNVDFDVVPEKYTIGATYAPE 121

RESULT 8
Q712N1_9POAL PRELIMINARY; PRT; 122 AA.
ID Q712N1_9POAL PRELIMINARY; PRT; 122 AA.
AC Q712N1_9POAL PRELIMINARY; PRT; 122 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Pollen allergen (Group II).
OS Lolium italicum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=85541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;

Query Match 57.0%; Score 292.5; DB 1; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKYPDGLTAEVLRHSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTMAEVELRHGSDWEVAMTKGEGVWTFDSEPL 86

QY 61 TGPNNFRFLSKGMKNVDFEVIPTAFTVGKTYTPE 95
DB 87 QGPFNFRFLTEKGMKNVDFDVVPEKYTIGATYAPE 121

RESULT 8
Q712N1_9POAL PRELIMINARY; PRT; 122 AA.
ID Q712N1_9POAL PRELIMINARY; PRT; 122 AA.
AC Q712N1_9POAL PRELIMINARY; PRT; 122 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Pollen allergen (Group II).
OS Lolium italicum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=85541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;

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RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131339; CAA10350.1; -; mRNA.
DR SMR; Q712N1; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen_Lolp2.
DR InterPro; IPR007117; Expan_Lol_pi_C.
DR Pfam; PF01357; Pollen_allerg_1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKYPDGLTAEVLRHSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTMAEVELRHGSDWEVAMTKGEGVWTFDSEPL 86

QY 61 TGPNNFRFLSKGMKNVDFEVIPTAFTVGKTYTPE 95
DB 87 QGPFNFRFLTEKGMKNVDFDVVPEKYTIGATYAPE 121

RESULT 9
Q712N2_WHEAT PRELIMINARY; PRT; 122 AA.
ID Q712N2_WHEAT PRELIMINARY; PRT; 122 AA.
AC Q712N2_WHEAT PRELIMINARY; PRT; 122 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Pollen allergen (Group II).
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131338; CAA10349.1; -; mRNA.
DR SMR; Q712N2; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen_Lolp2.
DR InterPro; IPR007117; Expan_Lol_pi_C.
DR Pfam; PF01357; Pollen_allerg_1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKYPDGLTAEVLRHSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTMAEVELRHGSDWEVAMTKGEGVWTFDSEPL 86

QY 61 TGPNNFRFLSKGMKNVDFEVIPTAFTVGKTYTPE 95
DB 87 QGPFNFRFLTEKGMKNVDFDVVPEKYTIGATYAPE 121

RESULT 10
Q712N3_POAPR PRELIMINARY; PRT; 122 AA.
ID Q712N3_POAPR PRELIMINARY; PRT; 122 AA.
AC Q712N3_POAPR PRELIMINARY; PRT; 122 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Pollen allergen (Group II).
OS Poa pratensis (Kentucky bluegrass).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaeae; Poa.
OX NCBI_TaxID=4545;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Sturaro M., Viotti A.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131337; CAA10348.1; -; mRNA.
DR SMR; Q712N3; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGMKNVDFEIVPTAFTVGTTYPE 95
DB 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 11
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ID Q712N4_HOLLA PRELIMINARY; PRT; 122 AA.
AC Q712N4_
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Pollen allergen (Group II).
OS Holcus lanatus (Velvet grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Holcus.
OX NCBI_TaxID=29679;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Sturaro M., Viotti A.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131336; CAA10347.1; -; mRNA.
DR SMR; Q712N4; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGMKNVDFEIVPTAFTVGTTYPE 95
DB 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 12
QY 712N4 HOLLA
ID Q712N4_HOLLA PRELIMINARY; PRT; 122 AA.
AC Q712N4_
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Pollen allergen (Group II).
OS Holcus lanatus (Velvet grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Holcus.
OX NCBI_TaxID=29679;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Sturaro M., Viotti A.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131336; CAA10347.1; -; mRNA.
DR SMR; Q712N4; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGMKNVDFEIVPTAFTVGTTYPE 95
DB 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 13
QY 712N4 HOLLA
ID Q712N4_HOLLA PRELIMINARY; PRT; 122 AA.
AC Q712N4_
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Pollen allergen (Group II).
OS Holcus lanatus (Velvet grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Holcus.
OX NCBI_TaxID=29679;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Sturaro M., Viotti A.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131336; CAA10347.1; -; mRNA.
DR SMR; Q712N4; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGMKNVDFEIVPTAFTVGTTYPE 95
DB 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

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ID Q9ZR00_CYNDA PRELIMINARY; PRT; 122 AA.
AC Q9ZR00_
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Pollen allergen (Group II).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poaceae; Chloridoideae; Cynodonteae; Cynodon.
OX NCBI_TaxID=28909;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Sturaro M., Viotti A.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131335; CAA10346.1; -; mRNA.
DR HSP; P43214; 1WHO.
DR SMR; Q9ZR00; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13332 MW; DFE63CB941C86B42 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGMKNVDFEIVPTAFTVGTTYPE 95
DB 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 13
QY 712N4 HOLLA
ID Q9ZR01_DACGL PRELIMINARY; PRT; 122 AA.
AC Q9ZR01_
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Pollen allergen (Group II).
OS Dactylis glomerata (Orchard grass) (Cock's-foot grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaeae; Dactylis.
OX NCBI_TaxID=4509;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Sturaro M., Viotti A.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131334; CAA10345.1; -; mRNA.
DR HSP; P43214; 1WHO.
DR SMR; Q9ZR01; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13332 MW; DFE63CADFE838B42 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKSGDAKTLVLNLIKTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
DB 29 KVTFTVEKSGNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGMKNVDFEIVPTAFTVGTTYPE 95
DB 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

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Db 29 KVTTFVEKGSNEKHLAVLVKY--EGDTMAEVELREHGSDEWVAMTKGGGVWTFDSEPL 86
Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTFTVGTYYTPE 95
Db 87 QGPFNFRFLTEKGMKNVDFDDVVPVKYITIGATYAPE 121

RESULT 14
Q40239 LOLPR PRELIMINARY; PRT; 88 AA.
AC Q40239;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Allergen Lol p II (Fragment)
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94012768; PubMed=7691817;
RA Sidoli A., Tamborini E., Giuntini I., Levi S., Volonte G., Pagni C.,
RA De Lalla C., Siccardi A.G., Baralle F.E., Galliani S., Acosio P.;
RT "Cloning, expression and immunological characterization of recombinant
RT Lolium perenne allergen Lol p II."
RL J. Biol. Chem. 268:21819-21825(1993).
DR EMBL; X73363; CAA51775.1; -; mRNA.
DR PIR; A48595; A48595.
DR HSP; P43214; 1BMW.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; LOP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
FT NON TER 1
FT NON TER 88
SQ SEQUENCE 88 AA; 9910 MW; 869139E7E0A5F88F CRC64;

Query Match 54.9%; Score 281.5; DB 2; Length 88;
Best Local Similarity 59.8%; Pred. No. 6.6e-23;
Matches 52; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy 4 DLTVEKGSDAKTLVNLINIKYTRPGDTLAEVELRQHGSEWEPMTKGN-LWEVKSAPLGT 62
Db 1 EFTVEKGSDEKNLSIKYKSGDAMAEVELKEHGSNEWLALKNGDGWWEIKSKDKPLKG 60

Qy 63 PNNFRFLSKGGMKNVDFEVIPTFTVGT 89
Db 61 PNFNFRVSEKGMNVDFDDVVPADFKVG 87

RESULT 15
Q8H7T4 ORYSA PRELIMINARY; PRT; 267 AA.
AC Q8H7T4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative beta-expansin.
GN Name=OSJNBa0009C08.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sasaki C.,
RA Currie J., Collura K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AC107224; AAN60490.1; -; Genomic_DNA.
DR HSP; P43213; 1N10.
DR SMR; Q8H7T4; 25-262.
DR Gramene; Q8H7T4; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016068; P:type I hypersensitivity; IEA.
DR InterPro; IPR005453; Allergen Lolp2.
DR InterPro; IPR007112; Expan endogl.
DR InterPro; IPR007118; Expan_Lol_pI.
DR InterPro; IPR007117; Expan_Lol_pI_C.
DR InterPro; IPR005132; Lipoprotein_13.
DR Pfam; PF03330; DPBB 1; 1.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01225; EXPANSIN_FAMLY.
DR PRINTS; PR01637; LOP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50843; EXPANSIN_EG45; 1.
SQ SEQUENCE 267 AA; 28937 MW; 69C86E6AD4DF40AB CRC64;

Query Match 32.7%; Score 167.5; DB 2; Length 267;
Best Local Similarity 35.4%; Pred. No. 8.1e-10;
Matches 34; Conservative 19; Mismatches 42; Indels 1; Gaps 1;

Qy 1 TKVDLTVEKGSDAKTLVNLINIKYTRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAP 59
Db 168 TKVTFHVEKGSNPNYFAVLVKYGGDGVVKVELKEGSEWKPINESWGAIWRIDTKP 227

Qy 60 LTGPMNFRFLSKGGMKNVDFEVIPTFTVGTYYTPE 95
Db 228 LKGFPSLRVTTESDQKLAVANDVIPDNWKANALYKSE 263

Search completed: February 16, 2006, 11:55:11
Job time : 244.744 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:56:20 ; Search time 196.487 Seconds
(without alignments)
206.270 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVEKGSDAKTLVNI.....FDEVIPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	100.0	97	3	US-09-847-208-114
2	513	100.0	97	4	US-10-628-296A-2
3	513	100.0	97	5	US-10-809-689-39
4	505	98.4	97	4	US-10-628-296A-4
5	433	84.4	96	4	US-10-628-296A-9
6	390	76.0	100	4	US-10-628-296A-13
7	367	71.5	97	4	US-10-628-296A-17
8	366	71.3	96	4	US-10-628-296A-18
9	312.5	60.9	97	3	US-09-847-208-113
10	312.5	60.9	97	5	US-10-809-689-38
11	307.5	59.9	96	4	US-10-628-296A-11
12	292.5	57.0	96	4	US-10-628-296A-15
13	282.5	57.0	122	3	US-09-847-208-139
14	282.5	57.0	122	5	US-10-809-689-53
15	287.5	56.0	94	3	US-09-957-806A-9
16	259.5	50.6	98	4	US-10-628-296A-14
17	232.5	45.3	98	4	US-10-628-296A-16
18	167.5	32.7	267	4	US-10-437-963-183122
19	166.5	32.5	226	4	US-10-437-963-197874
20	166.5	32.5	226	4	US-10-437-963-197877
21	166.5	32.5	269	4	US-10-425-115-270161
22	165	32.2	117	4	US-10-437-963-151767
23	164.5	32.1	270	4	US-10-425-115-197670
24	164.5	32.1	270	4	US-10-425-115-197673
25	164.5	32.1	270	4	US-10-425-115-197675
26	164.5	32.1	270	4	US-10-425-115-224320
27	164.5	32.1	276	4	US-10-425-114-52105

28	164	32.0	326	4	US-10-437-963-131483	Sequence 131483,
29	163.5	31.9	270	4	US-10-425-115-197668	Sequence 197668,
30	162.5	31.7	268	4	US-10-425-115-270166	Sequence 270166,
31	162	31.6	117	4	US-10-437-963-157987	Sequence 157987,
32	162	31.6	117	4	US-10-437-963-172999	Sequence 172999,
33	159.5	31.1	265	4	US-10-425-115-270164	Sequence 270164,
34	159.5	31.1	269	4	US-10-425-115-270162	Sequence 270162,
35	157	30.6	117	4	US-10-437-963-180827	Sequence 180827,
36	157	30.6	117	4	US-10-437-963-180828	Sequence 180828,
37	157	30.6	117	4	US-10-437-963-180829	Sequence 180829,
38	156	30.4	117	4	US-10-437-963-180824	Sequence 180824,
39	154	30.0	90	4	US-10-628-296A-10	Sequence 10, Appl
40	153.5	29.9	246	5	US-10-489-972-1	Sequence 1, Appl1
41	152.5	29.7	263	3	US-09-847-208-127	Sequence 127, App
42	151	29.4	118	4	US-10-437-963-186164	Sequence 186164,
43	149.5	29.1	263	3	US-09-811-672-10	Sequence 10, Appl
44	149.5	29.1	263	3	US-09-847-208-138	Sequence 138, App
45	149.5	29.1	263	4	US-10-245-871-193	Sequence 193, App

ALIGNMENTS

RESULT 1

US-09-847-208-114
; Sequence 114, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67 002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 97
; TYPE: PRP
; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-114

Query Match 100.0%; Score 513; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVNIKYTRPGDTLAEVELRQHGSSEWEPMTKKNLWEVKSAPKL 60

Db 1 TKVDLTVEKGSDAKTLVNIKYTRPGDTLAEVELRQHGSSEWEPMTKKNLWEVKSAPKL 60

Qy 61 TGPNNFRLSKGKMNVPFDEVIPTAFTVGKTYTPEYN 97

Db 61 TGPNNFRLSKGKMNVPFDEVIPTAFTVGKTYTPEYN 97

RESULT 2

US-10-628-296A-2
; Sequence 2, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 2
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-2

Query Match      100.0%; Score 513; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
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Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
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Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
    |||||||
Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
    |||||||

RESULT 3
US-10-689-689-39
; Sequence 39, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 39
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-39

Query Match      100.0%; Score 513; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
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Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
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Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
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RESULT 4
US-10-628-296A-4
; Sequence 4, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-4

Query Match      100.0%; Score 513; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
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Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
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Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
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Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
    |||||||

RESULT 5
US-10-628-296A-9
; Sequence 9, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-10-628-296A-9

Query Match      84.4%; Score 433; DB 4; Length 96;
Best Local Similarity 85.1%; Pred. No. 8.5e-43;
Matches 80; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 61
    |||||||
Db 2 KVTFKVEKGSDFKKLVLDIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 61
    |||||||

Qy 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPE 95
    |||||||
Db 62 GPFNFRFMSKGMKNVDFEVIPTAFTVGKITYTPE 95
    |||||||

RESULT 6
US-10-628-296A-13
; Sequence 13, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-13

Query Match      100.0%; Score 513; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
    |||||||
Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
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Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
    |||||||
Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKITYTPEYN 97
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-10-628-296A-13

Query Match          76.0%; Score 390; DB 4; Length 100;
Best Local Similarity 74.2%; Pred. No. 1e-37;
Matches 72; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 TKVOLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRQHGSEWEPMTKKGNLWEVKSAPL 60
Db 3 TKVKFTVQKGSDAKLVKIDYTRAGDTLSEMLRQHGSEWEPMFTTKGVDVWELSSKPL 62
QY 61 TGPMPFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
Db 63 VGPFNFRFLSKGGMKNVDFEVSFTDFKIGKTYEPTVD 99

RESULT 7
US-10-628-296A-17
; Sequence 17, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Triticum aestivum
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: X is unknown.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-628-296A-17

Query Match          71.5%; Score 367; DB 4; Length 97;
Best Local Similarity 70.5%; Pred. No. 4.9e-35;
Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRQHGSEWEPMTKKGNLWEVKSAPL 61
Db 3 RVKLAVEKGSDDKKLALKIDYTRPXDLSLEVELRQHGSEWEPMFTTKGVDVWELSSKPLV 62
QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 96
Db 63 GPFNFRFLSKGGMKNVDFEVSFTDFKIGKTYQPEY 97

RESULT 8
US-10-628-296A-18
; Sequence 18, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
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; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-628-296A-18

Query Match          71.3%; Score 366; DB 4; Length 96;
Best Local Similarity 70.5%; Pred. No. 6.3e-35;
Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 2 KYDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRQHGSEWEPMTKKGNLWEVKSAPL 61
Db 2 KVKLTVQKGSDDKKLALKIDYTRPNDLSLEVELRQYSEWQPLTKKGDVWELSSKPLV 61
QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 96
Db 62 GPFNFRFLSKGGMKNVDFEVSFTDFKIGKTYEPEY 96

RESULT 9
US-09-847-208-113
; Sequence 113, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-113

Query Match          60.9%; Score 312.5; DB 3; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-28;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

QY 3 VDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRQHGSEWEPMTKKGN-LWEVKSAPL 61
Db 4 VEFTVEKGSDEKNLALSIKYNKEGDSMAEVLKEHGSNEWLAKKNGDGVWEIKSDKPLK 63
QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 95
Db 64 GPFNFRFLSKGGMKNVDFDVDPADPKVGTGTYKPE 97

RESULT 10
US-10-809-689-38
; Sequence 38, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
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; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-38

Query Match          60.9%; Score 312.5; DB 5; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-28;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

QY      3 VDLTVEKGSDAKTLVNLNKYTRPGDTLAEVELRQHSGSEWEPMTKKGN-LWEVKSAKPLT 61
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       4 VFETVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKNGDGWWEIKSDKPLK 63
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      62 GPMNFRFLSKGGMKNVFDEVIPFTAFTVGKYTYPE 95
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       64 GPENFRFVSEKGMNRNFDDVPADFKVGTYYKPE 97
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-628-296A-11
; Sequence 11, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-11

Query Match          59.9%; Score 307.5; DB 4; Length 96;
Best Local Similarity 60.2%; Pred. No. 4.7e-28;
Matches 56; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

QY      3 VDLTVEKGSDAKTLVNLNKYTRPGDTLAEVELRQHSGSEWEPMTKKGN-LWEVKSAKPLT 61
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       4 VFETVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKNGDGWWEIKSDKPLK 63
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      62 GPMNFRFLSKGGMKNVFDEVIPFTAFTVGKYTPP 94
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       64 GPENFRFVSEKGMNRNFDDVPADFKVGTYYKP 96
        | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-10-628-296A-15
; Sequence 15, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
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GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:56:20 ; Search time 40.5128 Seconds
(without alignments)
206.270 Million cell updates/sec

Title: US-10-628-296A-5
Perfect score: 95
Sequence: 1 TKVDLTVEKGSDAKTLVNI 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	20	4	US-10-628-296A-5
2	95	100.0	97	3	US-09-847-208-114
3	95	100.0	97	4	US-10-628-296A-2
4	95	100.0	97	4	US-10-628-296A-4
5	95	100.0	97	5	US-10-809-689-39
6	69	72.6	100	4	US-10-628-296A-13
7	64	67.4	98	4	US-10-628-296A-14
8	59	62.1	96	4	US-10-628-296A-18
9	59	62.1	97	4	US-10-628-296A-17
10	58	61.1	96	4	US-10-628-296A-11
11	58	61.1	97	3	US-09-847-208-113
12	58	61.1	97	5	US-10-809-689-38
13	57	60.0	96	4	US-10-628-296A-9
14	55	57.9	36	3	US-09-847-208-71
15	50	52.6	98	4	US-10-628-296A-16
16	48	50.5	336	4	US-10-369-493-18524
17	47	49.5	611	6	US-11-097-143-11901
18	47	49.5	646	4	US-10-108-260A-2618
19	45	47.4	94	3	US-09-957-806A-9
20	45	47.4	96	4	US-10-628-296A-15
21	45	47.4	122	3	US-09-847-208-139
22	45	47.4	122	5	US-10-809-689-53
23	44	46.3	333	3	US-09-765-272-54
24	44	46.3	333	6	US-11-106-649-54
25	44	46.3	334	4	US-10-282-122A-51519
26	44	46.3	335	3	US-09-878-781-14
27	44	46.3	335	5	US-10-472-928-4188

28	44	46.3	336	3	US-09-878-766A-12	Sequence 12, Appl
29	44	46.3	336	3	US-09-878-766A-14	Sequence 14, Appl
30	44	46.3	336	3	US-09-878-781-4	Sequence 4, Appl
31	44	46.3	336	3	US-09-878-781-6	Sequence 6, Appl
32	44	46.3	336	4	US-10-134-297-4	Sequence 4, Appl
33	44	46.3	336	4	US-10-134-297-6	Sequence 6, Appl
34	44	46.3	336	4	US-10-282-122A-74379	Sequence 74379, A
35	44	46.3	336	4	US-10-650-369-12	Sequence 12, Appl
36	44	46.3	336	4	US-10-650-369-14	Sequence 14, Appl
37	44	46.3	336	6	US-11-005-508-4	Sequence 6, Appl
38	44	46.3	336	6	US-11-005-508-6	Sequence 6, Appl
39	44	46.3	336	6	US-11-066-594-12	Sequence 12, Appl
40	44	46.3	336	6	US-11-066-594-14	Sequence 14, Appl
41	44	46.3	337	4	US-10-282-122A-72254	Sequence 72254, A
42	44	46.3	345	5	US-10-474-792-550	Sequence 550, App
43	44	46.3	359	3	US-09-815-242-13169	Sequence 13169, A
44	44	46.3	359	3	US-09-815-242-13593	Sequence 13593, A
45	44	46.3	359	4	US-10-282-122A-74186	Sequence 74186, A

ALIGNMENTS

RESULT 1
US-10-628-296A-5
; Sequence 5, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-5

Query Match 100.0%; Score 95; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TKVDLTVEKGSDAKTLVNI 20
|||||
Db 1 TKVDLTVEKGSDAKTLVNI 20
|||||

RESULT 2
US-09-847-208-114
; Sequence 114, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne (Perennial ryegrass)

Query Match 100.0%; Score 95; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20: Conservative 0; Mismatches 0; Indels

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; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-628-296A-14

Query Match      67.4%; Score 64; DB 4; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.008;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 VDLTVEKSGDAKTLVLNI 20
Db      5 VSLTVEKSGDAKHLVLQI 22

RESULT 8
US-10-628-296A-18
; Sequence 18, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-628-296A-18

Query Match      62.1%; Score 59; DB 4; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.055;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 KVDLTVEKSGDAKTLVLNI 20
Db      2 KVKLTVEKSGDKKLALKI 20

RESULT 9
US-10-628-296A-17
; Sequence 17, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Triticum aestivum
; NAME/KEY: MISC FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: X is unknown.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-628-296A-17

Query Match      62.1%; Score 59; DB 4; Length 97;
Best Local Similarity 68.4%; Pred. No. 0.055;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 KVDLTVEKSGDAKTLVLNI 20
Db      3 RVKLTVEKSGDKKLALKI 21

RESULT 10
US-10-628-296A-11
; Sequence 11, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-11

Query Match      61.1%; Score 58; DB 4; Length 96;
Best Local Similarity 66.7%; Pred. No. 0.081;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 VDLTVEKSGDAKTLVLNI 20
Db      4 VFTVEKSGDEKNLALSI 21

RESULT 11
US-09-847-208-113
; Sequence 113, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: 198-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC57.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 97
; TYPE: PRT
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; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-113

Query Match 61.1%; Score 58; DB 3; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVNI 20
|:|||||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 12
US-10-809-689-38
; Sequence 38, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-38

Query Match 61.1%; Score 58; DB 5; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVNI 20
|:|||||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 13
US-10-628-296A-9
; Sequence 9, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-10-628-296A-9

Query Match 60.0%; Score 57; DB 4; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.12;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVKSGDAKTLVNI 20
|||:|||||||:|:|:

Db 2 KVTFFKVEKSGDPKKLVLDI 20

RESULT 14
US-09-847-208-71
; Sequence 71, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Dactylis glomerata (Orchard grass) (Cocksfoot grass)
US-09-847-208-71

Query Match 57.9%; Score 55; DB 3; Length 36;
Best Local Similarity 66.7%; Pred. No. 0.079;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVNI 20
|:|||||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 15
US-10-628-296A-16
; Sequence 16, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-10-628-296A-16

Query Match 52.6%; Score 50; DB 4; Length 98;
Best Local Similarity 61.1%; Pred. No. 1.9;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVNI 20
|:|||||||:|:|:
Db 5 VFTVEKSGSEKKLALQI 22

Search completed: February 16, 2006, 12:01:21
Job time : 41.5128 secs

; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-113

Query Match 61.1%; Score 58; DB 3; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVNI 20
|:|||||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 12
US-10-809-689-38
; Sequence 38, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-38

Query Match 61.1%; Score 58; DB 5; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVNI 20
|:|||||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 13
US-10-628-296A-9
; Sequence 9, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-10-628-296A-9

Query Match 60.0%; Score 57; DB 4; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.12;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVKSGDAKTLVNI 20
|||:|||||||:|:|:

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:35 ; Search time 45.812 Seconds
(without alignments)
191.818 Million cell updates/sec

Title: US-10-628-296A-5
Perfect score: 95
Sequence: 1 TKVDLTVEKSGDAKTLVLNI 20

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	20	8	ADJ65069 RyeGrass
2	95	100.0	97	2	AAY25600 Lolium sp
3	95	100.0	97	7	ADC34850 Rye grass
4	95	100.0	97	8	ADJ65066 RyeGrass
5	95	100.0	97	8	ADJ65068 RyeGrass
6	69	72.6	100	8	ADJ65077 Hordeum v
7	64	67.4	98	8	ADJ65078 Triticum
8	59	62.1	96	8	ADJ65082 Triticum
9	59	62.1	97	8	ADJ65081 Triticum
10	58	61.1	96	8	ADJ65075 Lolium pe
11	58	61.1	97	2	AAY25599 Lolium sp
12	58	61.1	97	7	ADC34849 Rye grass
13	57	60.0	96	8	ADJ65073 Dactylis
14	50	52.6	98	8	ADJ65080 Hordeum v
15	49.5	52.1	837	6	ABU63527 Malignant
16	48	50.5	336	5	ABBS5601 Lactococ
17	48	50.5	336	8	ADS29491 Bacterial
18	47	49.5	611	4	ABB61703 Drosophil
19	47	49.5	646	7	ADM03933 Human pro
20	46	48.4	909	3	AAG53638 Arabidops
21	46	48.4	987	3	AAG53637 Arabidops
22	46	48.4	1020	3	AAG53636 Arabidops
23	45	47.4	34	8	ADQ76059 Phl p 2 m
24	45	47.4	94	4	ABM00018 Allergen

25	45	47.4	96	8	ADJ65079 Phleum pr
26	45	47.4	103	8	ADQ76057 Phl p 2 m
27	45	47.4	122	2	AAR63207 Recombina
28	45	47.4	122	2	AAY25614 Phleum sp
29	45	47.4	122	7	ADC34864 Timothy g
30	44	46.3	216	4	AU42604 Propionib
31	44	46.3	216	6	ABM39123 Propionib
32	44	46.3	298	8	ADV89261 Streptoco
33	44	46.3	298	8	ADV80514 Streptoco
34	44	46.3	333	2	AAW55089 Streptoco
35	44	46.3	333	5	ABP54583 S. pneumo
36	44	46.3	333	7	ADC45135 S. pneumo
37	44	46.3	334	6	ABU23595 Protein e
38	44	46.3	335	6	ABU02516 S. pneumo
39	44	46.3	336	2	AAR56486 Plasmid r
40	44	46.3	336	4	AAY85681 Streptoco
41	44	46.3	336	5	ABP30758 Streptoco
42	44	46.3	336	5	ABP29960 Streptoco
43	44	46.3	336	5	AAW50666 Streptoco
44	44	46.3	336	5	AAW50665 Streptoco
45	44	46.3	336	5	AAW50639 Streptoco

ALIGNMENTS

RESULT 1

ADJ65069
ID ADJ65069 standard; peptide; 20 AA.
XX
AC ADJ65069;
XX
DT 06-MAY-2004 (first entry)
XX
DE RyeGrass Lol p 3 allergen N-terminal peptide SEQ ID NO:5.
XX
KW allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
KW ryeGrass; Lol p 3.
XX
OS Lolium perenne.
XX
FN WO2004011025-A1.
XX
PD 05-FEB-2004.
XX
PF 28-JUL-2003; 2003WO-US023600.
XX
PR 29-JUL-2002; 2002US-0399688P.
XX (PENN-) PENN STATE RES FOUND.
XX
PI Li L, Cosgrove D;
XX
DR WPI; 2004-143737/14.
XX
PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.
XX
PS Disclosure; SEQ ID NO 5; 73pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing

CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (f) The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents a ryegrass
CC Lol p 3 allergen N-terminal peptide, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 95; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. NO. 3.2e-09; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
| | | | | | | | | | | | | | | | | | | |
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 2
AAV25600
ID AAV25600 standard; protein; 97 AA.
AC AAV25600;
XX
XX
DT 30-SEP-1999 (first entry)
XX
DE Lolium sp. allergen 126387 Lol p 3 protein fragment.
XX
KW Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
OS Lolium sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-GB000080.
XX
XX 09-JAN-1998; 98GB-00000445.
XX
XX 21-SEP-1998; 98GB-00020474.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Larche M, Kay AB;
XX
XX WPI; 1999-458255/38.
XX
XX Desensitizing patients to polypeptide allergens.
XX
XX Example 6; Page 55; 117pp; English.
XX
XX This invention describes a novel method of desensitizing a patient to a
XX polypeptide allergen and comprises administering to the patient a peptide
XX derived from the allergen where restriction to a MHC Class II molecule
XX possessed by the patient can be demonstrated for the peptide and the
XX peptide is able to induce a late phase response in an individual who

CC possesses the MHC Class II molecule. The methods can be used for
CC desensitising patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chiromidae (non-biting midges), spiders and mites, housefly, fruit
CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, of
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents the Lolium sp. allergen 126385 Lol p 2a
XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 95; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. NO. 2.1e-08; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
| | | | | | | | | | | | | | | | | | | |
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 3
ADC34850
ID ADC34850 standard; protein; 97 AA.
XX
AC ADC34850;
XX
DT 18-DEC-2003 (first entry)
XX
DE Rye grass allergen Lol p 3.
XX
KW rye grass; allergen; antigen; hyporesponsive; desensitisation;
KW immunomodulator; gene therapy.
XX
OS Lolium sp.
XX
PN WO2003047618-A2.
XX
XX 12-JUN-2003.
XX
XX 05-DEC-2002; 2002WO-GB005548.
XX
XX 05-DEC-2001; 2001US-0338385P.
XX
XX (CIRC-) CIRCASSIA LTD.
XX
XX Larche M, Ledger PW;
XX
XX WPI; 2003-523267/49.
XX
XX Desensitizing an individual to a selected polypeptide antigen comprises
XX administering a composition containing polypeptide antigens in an amount
XX that generates a state of hyporesponsiveness to the antigen to allow
XX desensitization.
XX
XX Disclosure; Page 25; 57pp; English.
XX
XX The invention relates to a novel method for desensitising an individual
XX to a selected polypeptide antigen. The method comprises administering a
XX composition that contains polypeptide antigens in an amount that
XX generates in the individual a state of hyporesponsiveness to the antigen
XX to allow desensitisation to one or more polypeptide antigens. The method
XX of the invention has immunomodulator activity, and may have a use in gene
XX therapy. The composition and method are useful in manufacturing a
XX medicament for desensitising an individual to a selected polypeptide
XX antigen or for generating in the individual a state of hyporesponsiveness
XX to the antigen to allow desensitisation to one or more polypeptide
XX antigens. The present sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 97 AA;

Query Match 100.0%; Score 95; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKSGDAKTLVLNI 20
|||
Db 1 TKVDLTVEKSGDAKTLVLNI 20

RESULT 4
ADJ65066
ID ADJ65066 standard; protein; 97 AA.
XX AC ADJ65066;
XX DT 06-MAY-2004 (first entry)
XX DE Ryegrass Lol p 3 allergen protein SEQ ID NO:2.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
KW ryegrass; Lol p 3.
XX OS Lolium perenne.
PN WO2004011025-A1.
XX PD 05-FEB-2004.
PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX WPI; 2004-143737/14.
DR N-PSDB; ADJ65065.
XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.
XX Claim 6; SEQ ID NO 2; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues

CC in which they are expressed. The present sequence represents the ryegrass
CC Lol p 3 allergen, which is used in the exemplification of the present
CC invention.
XX Sequence 97 AA;
Query Match 100.0%; Score 95; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKSGDAKTLVLNI 20
|||
Db 1 TKVDLTVEKSGDAKTLVLNI 20

RESULT 5
ADJ65068
ID ADJ65068 standard; protein; 97 AA.
XX AC ADJ65068;
XX DT 06-MAY-2004 (first entry)
XX DE Ryegrass Lol p 3 allergen modified variant protein SEQ ID NO:4.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
KW ryegrass; Lol p 3; modified; variant.
XX OS Lolium perenne.
OS Synthetic.
PN WO2004011025-A1.
XX PD 05-FEB-2004.
XX PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX WPI; 2004-143737/14.
XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.
XX Disclosure; SEQ ID NO 4; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent

CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (1) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC in which they are expressed. The present sequence represents a modified
CC variant ryegrass Lol p 3 allergen protein sequence, which is used in the
CC exemplification of the present invention.

XX Sequence 97 AA;

Query Match 100.0%; Score 95; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNI 20
|||||
Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 6

ADJ65077
ID ADJ65077 standard; protein; 100 AA.

XX AC ADJ65077;

XX DT 06-MAY-2004 (first entry)

XX DE Hordeum vulgare allergen amino acid sequence SEQ ID NO:13.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;

XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Hordeum vulgare.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 13; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (1)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (1); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that

CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (1) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 100 AA;

Query Match 72.6%; Score 69; DB 8; Length 100;
Best Local Similarity 75.0%; Pred. No. 0.00076;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNI 20
|||||
Db 3 TKVKFTVQKGSDAKKLVLI 22
|||

RESULT 7

ADJ65078

ID ADJ65078 standard; protein; 98 AA.

XX AC ADJ65078;

XX DT 06-MAY-2004 (first entry)

XX DE Triticum aestivum allergen amino acid sequence SEQ ID NO:14.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;

XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Triticum aestivum.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 14; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (1)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (1); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC producing a polypeptide having expansin activity; (10) a transgenic plant

CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridizes to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 98 AA;

Query Match 67.4%; Score 64; DB 8; Length 98;
 Best Local Similarity 77.8%; Pred. No. 0.0055;
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VDLTVEKSGDAKTIVLNI 20
 | : ||||| ||||| |||||
 Db 5 VSITVEKSGDAKHLVLQI 22

RESULT 8

ADJ65082
 ID ADJ65082 standard; protein; 96 AA.

XX AC ADJ65082;

XX DT 06-MAY-2004 (first entry)

XX XX Triticum aestivum allergen amino acid sequence SEQ ID NO:18.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Triticum aestivum.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX DR WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
 XX PT activity, useful for altering plant cell wall properties to effect
 XX PT growth, flexibility and mechanical strength in tissues in which they are
 XX PT expressed.

XX PS Claim 6; SEQ ID NO 18; 73pp; English.

XX XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (iii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (i);
 CC (6) an antibody that selectively binds to (iv); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridizes to S1 under stringent conditions; (8) a method of

CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridizes to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 96 AA;

Query Match 62.1%; Score 59; DB 8; Length 96;
 Best Local Similarity 68.4%; Pred. No. 0.04;
 Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGSDAKTIVLNI 20
 ||| : ||||| ||||| |||||
 Db 2 KVKLTVEKSGSDKKKTLAKI 20

RESULT 9

ADJ65081

ID ADJ65081 standard; protein; 97 AA.

XX AC ADJ65081;

XX XX 06-MAY-2004 (first entry)

XX DE Triticum aestivum allergen amino acid sequence SEQ ID NO:17.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Triticum aestivum.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX DR WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
 XX PT activity, useful for altering plant cell wall properties to effect
 XX PT growth, flexibility and mechanical strength in tissues in which they are
 XX PT expressed.

XX PS Claim 6; SEQ ID NO 17; 73pp; English.

XX XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (iii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (i);
 CC (6) an antibody that selectively binds to (iv); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells

CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method for
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC in which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX Sequence 97 AA;

Query Match 62.1%; Score 59; DB 8; Length 97;

Best Local Similarity 68.4%; Pred. No. 0.041;

Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVLNI 20

Db 3 RVKLTVEKGSDDKKLALKI 21

RESULT 10

ADJ65075

ID ADJ65075 standard; protein; 96 AA.

AC ADJ65075;

XX 06-MAY-2004 (first entry)

DT

XX

DE Lolium perenne allergen amino acid sequence SEQ ID NO:11.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX Lolium perenne.

OS

PN WO2004011025-A1.

XX

PD 05-FEB-2004.

XX

PF 28-JUL-2003; 2003WO-US023600.

XX

PR 29-JUL-2002; 2002US-0399688P.

XX

PA (PENN-) PENN STATE RES FOUND.

XX

PI Li L, Cosgrove D;

XX

DR WPI; 2004-143737/14.

XX

PT New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX

PS Claim 6; SEQ ID NO 11; 73pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
 CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
 CC (6) an antibody that selectively binds to (IV); (7) a method of modifying

CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method for
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC in which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

Query Match 61.1%; Score 58; DB 8; Length 96;

Best Local Similarity 66.7%; Pred. No. 0.06;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVEKGSDAKTLVLNI 20

Db 4 VEFTVEKGSDEKNLALSI 21

RESULT 11

AAY25599

ID AAY25599 standard; protein; 97 AA.

XX

AC AAY25599;

XX

DT 30-SEP-1999 (first entry)

XX

DE Lolium sp. allergen 126386 Lol p 2a protein fragment.

XX

KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX

OS Lolium sp.

XX

PN WO9934826-A1.

XX

PD 15-JUL-1999.

XX

PF 11-JAN-1999; 99WO-GB0000080.

XX

PR 09-JAN-1998; 98GB-00000445.

XX

PR 21-SEP-1998; 98GB-00020474.

XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX

PI Larche M, Kay AB;

XX

DR WPI; 1999-458255/38.

XX

PT Desensitizing patients to polypeptide allergens.

XX

PS Example 6; Page 55; 117pp; English.

XX

CC This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who

CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitising patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents the Lolium sp. allergen 126385 Lol p 2a

XX Sequence 97 AA;

Query Match 61.1%; Score 58; DB 2; Length 97;
 Best Local Similarity 66.7%; Pred. No. 0.061;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
 | : ||||| | : |
 Db 4 VEFTVEKSGDEKNLALS I 21

RESULT 12
 ADC34849
 ID ADC34849 standard; protein; 97 AA.

XX AC ADC34849;

XX DT 18-DEC-2003 (first entry)

XX DE Rye grass allergen Lol p 2a.

XX KW rye grass; allergen; antigen; hyporesponsive; desensitisation;
 KW immunomodulator; gene therapy.

XX OS Lolium sp.

XX PN WO2003047618-A2.

XX PD 12-JUN-2003.

XX PF 05-DEC-2002; 2002WO-GB005548.

XX PR 05-DEC-2001; 2001US-0338385P.

XX PA (CIRC-) CIRCASSIA LTD.

XX PI Larche M, Ledger PW;

XX DR WPI; 2003-523267/49.

XX Desensitising an individual to a selected polypeptide antigen comprises
 PT administering a composition containing polypeptide antigens in an amount
 PT that generates a state of hyporesponsiveness to the antigen to allow
 PT desensitization.

XX Disclosure; Page 25; 57pp; English.

XX The invention relates to a novel method for desensitising an individual
 CC to a selected polypeptide antigen. The method comprises administering a
 CC composition that contains polypeptide antigens in an amount that
 CC generates in the individual a state of hyporesponsiveness to the antigen
 CC to allow desensitisation to one or more polypeptide antigens. The method
 CC of the invention has immunomodulator activity, and may have a use in gene
 CC therapy. The composition and method are useful in manufacturing a
 CC medicament for desensitising an individual to a selected polypeptide
 CC antigen or for generating in the individual a state of hyporesponsiveness
 CC to the antigen to allow desensitisation to one or more polypeptide
 CC antigens. The present sequence is used in the exemplification of the
 CC invention.

XX Sequence 97 AA;

Query Match 61.1%; Score 58; DB 7; Length 97;
 Best Local Similarity 66.7%; Pred. No. 0.061;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
 | : ||||| | : |
 Db 4 VEFTVEKSGDEKNLALS I 21

RESULT 13
 ADJ65073
 ID ADJ65073 standard; protein; 96 AA.

XX AC ADJ65073;

XX DT 06-MAY-2004 (first entry)

XX DE Dactylis glomerata allergen amino acid sequence SEQ ID NO:9.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Dactylis glomerata.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX DR WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX Claim 6; SEQ ID NO 9; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (i);
 CC (6) an antibody that selectively binds to (iv); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method of
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (i) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

Qy 1 TKVDLTVEKGSDAKTLVLN 19
||:| :|:| :|:| :|:|
Db 211 TKIDL-MDKGADASKMLN 228

Search completed: February 16, 2006, 11:50:13
Job time : 46.812 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:50:34 ; Search time 39.7949 Seconds
(without alignments)
234.528 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVEKGSADKTLVNI.....FDEVIPTFTVGKTYTPEYN 97

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	100.0	97	2 A33422	allergen Lol pIII
2	366	71.3	118	2 T06550	pollen allergen ho
3	312.5	60.9	97	2 A34291	pollen allergen Lo
4	282.5	57.0	122	2 S39457	pollen allergen Ph
5	272.5	53.1	88	2 A48595	major allergen Lol
6	152.5	29.7	263	2 T03303	major allergen Ory
7	149.5	29.1	263	2 S44182	allergen Phl p I -
8	144.5	28.2	263	2 B37881	pollen allergen Lo
9	143	27.9	262	2 S38620	allergen Phl pI -
10	139.5	27.2	265	2 S38581	allergen Hol I i p
11	135.5	26.4	263	2 S13614	major allergen Lol
12	126.5	24.7	191	2 G1524	major allergen mi
13	103.5	20.2	277	2 S48032	cim1 protein - soy
14	102.5	20.0	491	2 F96681	protein FlE22.6 (i
15	98	19.1	261	2 T04301	beta-expansin - ri
16	92.5	18.0	252	2 T47868	hypothetical prote
17	87	17.0	258	2 T10083	expansin S2 precu
18	83.5	16.3	265	2 T05668	pollen allergen ho
19	82.5	16.1	259	2 T50657	beta-expansin (imp
20	82.5	16.1	271	2 H84592	beta-expansin (imp
21	77	15.0	265	2 T47537	hypothetical prote
22	75.5	14.7	259	2 B84886	probable beta-expa
23	74.5	14.5	263	2 T47536	hypothetical prote
24	72	14.0	645	2 H90801	hypothetical prote
25	72	14.0	711	2 G85610	hypothetical prote
26	72	14.0	735	2 T49622	hypothetical prote
27	71	13.8	283	2 AF3180	agrobacterium viru
28	71	13.8	411	2 T49928	beta-glucosidase-1
29	70.5	13.7	720	2 A36942	Fe(III)-pyochelin

30 69.5 13.5 161 2 A64993
31 69.5 13.5 2254 2 D86215
32 68 13.3 840 2 G72468
33 68 13.3 1377 2 C70148
34 67.5 13.2 1154 2 S43275
35 67.5 13.2 1534 2 A85862
36 67.5 13.2 1534 2 G91017
37 67 13.1 522 2 T23458
38 67 13.1 2747 2 B49132
39 66.5 13.0 371 2 D82031
40 66.5 13.0 500 2 A83617
41 66 12.9 536 2 T04998
42 65.5 12.8 293 2 T08115
43 65.5 12.8 581 2 T29096
44 65.5 12.8 609 2 A30894
45 65 12.7 178 2 AHI330

ALIGNMENTS

RESULT 1

A33422

allergen Lol pIII - perennial ryegrass

C:Species: Lolium perenne (perennial ryegrass)

C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 31-Dec-2004

C:Accession: A33422

R:Ansari, A. A.; Shenbagamurthi, P.; Marsh, D. G.

Biochemistry 28, 8665-8670, 1989

Artifite: Complete primary structure of a Lolium perenne (Perennial rye grass) pollen all

A:Reference number: A33422; MUID:90105394; PMID:2605214

A:Accession: A33422

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-97 <ANS>

A:Cross-references: UNIPROT:P14948; UNIPARC:UPI00000004DD9

C:Superfamily: Pollen allergen, Group II

C:Keywords: pollen

Query Match 100.0%; Score 513; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 1.2e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 97; Conservative 0;

Qy 1 TKVDLTVEKGSADKTLVNIKYTPGDTLAELVLRQHGSEEWPMTKGNLWEVKSAPL 60

Db 1 TKVDLTVEKGSADKTLVNIKYTPGDTLAELVLRQHGSEEWPMTKGNLWEVKSAPL 60

Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTFTVGKTYTPEYN 97

Db 61 TGPNNFRFLSKGGMKNVDFEVIPTFTVGKTYTPEYN 97

RESULT 2

T06550

pollen allergen homolog - wheat

C:Species: Triticum aestivum (common wheat)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004

C:Accession: T06550

R:Baizer, H.J.

submitted to the EMBL Data Library, August 1995

A:Reference number: Z15755

A:Accession: T06550

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-118 <BAL>

A:Cross-references: UNIPROT:Q41576; UNIPARC:UPI000000A6E33; EMBL:Z50867; NID:g972512; PID:

A:Experimental source: var. Salmon; developmental stage anthesis; Gynoecia

C:Superfamily: Pollen allergen, Group II

C:Keywords: pollen

Query Match 71.3%; Score 366; DB 2; Length 118;

Best Local Similarity 70.5%; Pred. No. 3.7e-31;

Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Tue Feb 21 09:20:30 2006

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major allergen Lol p II - perennial ryegrass (fragment)
C:Species: Lolium perenne (perennial ryegrass)
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A48595
J:Sidoli, A.; Tamborini, E.; Giuntini, I.; Levi, S.; Volonte, G.; Paini, C.; De Lalla, C.
R: Biol. Chem. 268, 21819-21825, 1993
A:Title: Cloning, expression, and immunological characterization of recombinant Lolium p
A:Reference number: A48595, MUID:94012768; PMID:7691817
A:Accession: A48595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-88 <SID>
A:Cross-references: UNIPROT:Q40239; UNIPARC:UPI000017999D
A:Experimental source: pollen
A>Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:138591, NCBIPI:138592)
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match      53.1%; Score 272.5; DB 2; Length 88;
Best Local Similarity 58.6%; Pred. No. 1.6e-21;
Matches 51; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

Qy      4 DLTVEKSGDAKTLVLNIKYTRPGDTLAEVLRLQHGSEEWPMYTKGN-LWEVKSAKPLTG 62
Db      1 EFTVEKSGDEKNLALSIKYKNGEGDMAEVELKEHGSNEWLAKKNGDGVWEIKSDKPLKG 60

Qy      63 PMNFRFLSKGGMKNVDFEVIPTAFTVG 89
Db      61 PFNFRFVSEKGMNVFDDVVPADPKVG 87

RESULT 6
T03303
major allergen Ory s 1 - rice
C:Species: Oryza sativa (rice)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C:Accession: T03303
Gene 164, 255-259, 1995
R:Xu, H.; Theerakulpisut, P.; Goulding, N.; Suphioglu, C.; Singh, M.B.; Bhalla, P.L.
A:Title: Cloning, expression and immunological characterization of Ory s 1, the major al
A:Reference number: Z14899; MUID:96069591; PMID:7590339
A:Accession: T03303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-263 <XOR>
A:Cross-references: UNIPROT:Q40638; UNIPARC:UPI000012F49C; EMBL:U31771; NID:G1173556; PI

Query Match      29.7%; Score 152.5; DB 2; Length 263;
Best Local Similarity 33.3%; Pred. No. 2.1e-08;
Matches 28; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

Qy      1 TKVDLTVEKSGDAKTLVLNIKYTRPGDTLAEVLRLQHGSEEWPMYTKGN-LWEVKSAKPL 59
Db      165 TKITTHIEKASNPYLLLVKYGAGDGVVEIKEGSEEWKALKESGAIWRIDTPKP 224

Qy      60 LTGPMNFRFLSKGGMKNVDFEVIPT 83
Db      225 LKGPFSVRVTTEGARRSAEDAIP 248

RESULT 7
S44182
allergen Phl p I - common timothy
C:Species: Phleum pratense (common timothy)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Dec-2004
C:Accession: S44182
R:Laffer, S.; Valenta, R.; Vrtala, S.; Suesani, M.; van Ree, R.; Kraft, D.; Scheiner, O.
A:Title: Molecular characterization of Phl p I, a major timothy grass (Phleum pra
A:Reference number: S39457; MUID:94085541; PMID:8262175
A:Accession: S39457
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <DOL>
A:Cross-references: UNIPROT:P43214; UNIPARC:UPI0000000331; EMBL:X75925; NID:G415895; PID
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match      57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 1.9e-23;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

Qy      2 KYDLTVEKSGDAKTLVLNIKYTRPGDTLAEVLRLQHGSEEWPMYTKGN-LWEVKSAKPL 60
Db      29 KYTFTVEKSGNEKHLAVLKY--EGDTMAEVLRLQHGSEEWPMYTKGEGGVWTFDSEEP 86

Qy      61 TGPMMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db      87 QGPFNFRFLTEKGMKNVDFDDVVPADPKVGTTYKPE 121

RESULT 5
A48595

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major allergen Lol p II - perennial ryegrass (fragment)
C:Species: Lolium perenne (perennial ryegrass)
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A48595
J:Sidoli, A.; Tamborini, E.; Giuntini, I.; Levi, S.; Volonte, G.; Paini, C.; De Lalla, C.
R: Biol. Chem. 268, 21819-21825, 1993
A:Title: Cloning, expression, and immunological characterization of recombinant Lolium p
A:Reference number: A48595, MUID:94012768; PMID:7691817
A:Accession: A48595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-88 <SID>
A:Cross-references: UNIPROT:Q40239; UNIPARC:UPI000017999D
A:Experimental source: pollen
A>Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:138591, NCBIPI:138592)
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match      53.1%; Score 272.5; DB 2; Length 88;
Best Local Similarity 58.6%; Pred. No. 1.6e-21;
Matches 51; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

Qy      4 DLTVEKSGDAKTLVLNIKYTRPGDTLAEVLRLQHGSEEWPMYTKGN-LWEVKSAKPLTG 62
Db      1 EFTVEKSGDEKNLALSIKYKNGEGDMAEVELKEHGSNEWLAKKNGDGVWEIKSDKPLKG 60

Qy      63 PMNFRFLSKGGMKNVDFEVIPTAFTVG 89
Db      61 PFNFRFVSEKGMNVFDDVVPADPKVG 87

RESULT 6
T03303
major allergen Ory s 1 - rice
C:Species: Oryza sativa (rice)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C:Accession: T03303
Gene 164, 255-259, 1995
R:Xu, H.; Theerakulpisut, P.; Goulding, N.; Suphioglu, C.; Singh, M.B.; Bhalla, P.L.
A:Title: Cloning, expression and immunological characterization of Ory s 1, the major al
A:Reference number: Z14899; MUID:96069591; PMID:7590339
A:Accession: T03303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-263 <XOR>
A:Cross-references: UNIPROT:Q40638; UNIPARC:UPI000012F49C; EMBL:U31771; NID:G1173556; PI

Query Match      29.7%; Score 152.5; DB 2; Length 263;
Best Local Similarity 33.3%; Pred. No. 2.1e-08;
Matches 28; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

Qy      1 TKVDLTVEKSGDAKTLVLNIKYTRPGDTLAEVLRLQHGSEEWPMYTKGN-LWEVKSAKPL 59
Db      165 TKITTHIEKASNPYLLLVKYGAGDGVVEIKEGSEEWKALKESGAIWRIDTPKP 224

Qy      60 LTGPMNFRFLSKGGMKNVDFEVIPT 83
Db      225 LKGPFSVRVTTEGARRSAEDAIP 248

RESULT 7
S44182
allergen Phl p I - common timothy
C:Species: Phleum pratense (common timothy)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Dec-2004
C:Accession: S44182
R:Laffer, S.; Valenta, R.; Vrtala, S.; Suesani, M.; van Ree, R.; Kraft, D.; Scheiner, O.
A:Title: Molecular characterization of Phl p I, a major timothy grass (Phleum pra
A:Reference number: S44182
A:Accession: S44182
A:Status: preliminary

```


R;Esch, R.E.; Klapper, D.G.
Mol. Immunol. 26, 557-561, 1989
A:Title: Isolation and characterization of a major cross-reactive grass group I allergen
A:Reference number: A37396; MUID:89364850; PMID:2475768
A:Accession: A37396
A:Status: preliminary
A:Molecule type: protein
A:Residues: 236-263 <ESC>
A:Cross-references: UNIPARC:UPI0000143439
C:Keywords: pollen

Query Match 26.4%; Score 135.5; DB 2; Length 263;
Best Local Similarity 27.7%; Pred. No. 1.2e-06;
Matches 26; Conservative 24; Mismatches 43; Indels 1; Gaps 1;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAP 59
Db 168 TKTPHVEKASPNVLAIVLVKVDGDDVAVDIKEKGDKWIELKESWGAVWRIDTPDK 227

QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 228 LTGPFTVYRTGGTKSEVEDVIPEGWKADTSYS 261

RESULT 12
JCI524
major allergen m1 protein - maize
C:Species: Zea mays (maize)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Dec-2004
C:Accession: JCI524
R:Broadwater, A.H.; Rubinstein, A.L.; Chay, C.H.; Klapper, D.G.; Bedinger, P.A.
Gene 131, 227-230, 1993
A:Title: Zea m1, the maize homolog of the allergen-encoding Lol pI gene of rye grass.
A:Reference number: JCI524; MUID:94010312; PMID:8406014
A:Accession: JCI524
A:Molecule type: mRNA
A:Residues: 1-191 <BRO>
A:Cross-references: UNIPROT:Q07154; UNIPARC:UPI000012A33E; GB:L14271; NID:g293901; PIDN:
A:Experimental source: pollen
A:Note: the authors translated the codon GTG for residue 107 as Leu
C:Genetics:
A:Gene: Zea m1
C:Superfamily: Major pollen allergen/expansion
C:Keywords: pollen

Query Match 24.7%; Score 126.5; DB 2; Length 191;
Best Local Similarity 28.0%; Pred. No. 7.4e-06;
Matches 26; Conservative 21; Mismatches 45; Indels 1; Gaps 1;

QY 2 KVDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAPL 60
Db 93 KIVFHIEKGCNPNYAVLVKVFVADGDGDIVLMBEIQDKLSAEWKPMKLSWGAIWRMDTAKAL 152

QY 61 TGPMMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 153 KGFFSIRLTSESGKVKIAKDIIIPANWRPDAVTT 185

RESULT 13
S48032
c1m1 protein - soybean
C:Species: Glycine max (soybean)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 31-Dec-2004
C:Accession: S48032
R:Crowell, D.N.
Plant Mol. Biol. 25, 829-835, 1994
A:Title: Cytokinin regulation of a soybean pollen allergen gene.
A:Reference number: S48032; MUID:94355655; PMID:8075399
A:Accession: S48032
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <CRO>
A:Cross-references: UNIPROT:Q39802; UNIPARC:UPI00000A3031; EMBL:U03860; NID:g555615; PID

C:Superfamily: Major pollen allergen/expansion

Query Match 20.2%; Score 103.5; DB 2; Length 277;
Best Local Similarity 29.2%; Pred. No. 0.0029;
Matches 26; Conservative 19; Mismatches 41; Indels 3; Gaps 3;

QY 7 VEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAPLTPGM 64
Db 181 VDSGSNQEYPATLVEYEDGDLAKVELKDALDSSWDSMQSGWGVWFKDGSPLRAPF 240

QY 65 NFRFLS-KGGMKNVDFEVIPTAFTVGKTY 92
Db 241 SIKLTLESQTIVANNVIPAGWTPGQTY 269

RESULT 14
F96681
protein FIE22.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96681
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Creasy, A.R.; Conway, A.B.; Huizar, L.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96681
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-491 <STO>
A:Cross-references: UNIPARC:UPI00001608B5; GB:AE005173; NID:g6686395; PIDN:AAF23829.1; P
C:Genetics:
A:Gene: FIE22.6
A:Map position: 1

Query Match 20.0%; Score 102.5; DB 2; Length 491;
Best Local Similarity 28.9%; Pred. No. 0.0073;
Matches 26; Conservative 20; Mismatches 41; Indels 3; Gaps 3;

QY 3 VDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAPL 60
Db 175 VTFQVDKGSNANSFAVLVAYYNGDGEIGRIELKQALDSKWLMSQSGWGVWFKLDVSSPL 234

QY 61 TGPMMNFRFLS-KGGMKNVDFEVIPTAFTVG 89
Db 235 RAPLSRVTLSLESGKTVVASNVIPANWQPG 264

RESULT 15
T04301
beta-expansin - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C:Accession: T04301
R:Cosgrove, D.J.; Bedinger, P.; Durachko, D.M.
Proc. Natl. Acad. Sci. U.S.A. 94, 6559-6564, 1997
A:Title: Group I allergens of grass pollen as cell wall-loosening agents.
A:Reference number: Z15266; MUID:97322412; PMID:9177257
A:Accession: T04301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-261 <COS>
A:Cross-references: UNIPROT:Q24230; UNIPARC:UPI000009E4F4E; EMBL:U95968; NID:g2224914; P
C:Superfamily: Major pollen allergen/expansion

Query Match 19.1%; Score 98; DB 2; Length 261;
Best Local Similarity 22.9%; Pred. No. 0.01;

Matches 22; Conservative 24; Mismatches 44; Indels 6; Gaps 2;
QY 3 VDLTVEKGSDAKTLVLNLIKVTREGDTLAEVELRQ-----HGSEWEPMTKK-GNLWEVKS 56
|: |||: | : : : | : : : : | : : : : | : : : :
Db 159 VNFHVEAGSNPVYLAFLVEFANKDGTVVQLDVWESLPSGKPTRVWTPMRRSWGSIWRLLDA 218
|: |||: | : : : | : : : : | : : : : | : : : :
QY 57 AKPLTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTY 92
|: |||: | : : : | : : : : | : : : : | : : : :
Db 219 NHRLOGPXSLRMVSESGQTIVIAHQVIPANWRANTNY 254
|: |||: | : : : | : : : : | : : : : | : : : :

Search completed: February 16, 2006, 11:56:04
Job time : 40.7949 secs

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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:57:35 ; Search time 17.4103 Seconds
(without alignments)
79.196 Million cell updates/sec

Title: US-10-628-296A-2
Perfect score: 513
Sequence: 1 TKVDLTVEKGSDAKTLVLMNI.....FDEVIPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
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2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
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8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	513	100.0	97	6	US-10-498-026-33
2	312.5	60.9	97	6	US-10-498-026-32
3	292.5	57.0	122	6	US-10-498-026-47
4	149.5	29.1	263	6	US-10-498-026-45
5	149.5	29.1	263	7	US-11-033-039-193
6	143	27.9	262	6	US-10-498-026-46
7	142.5	27.8	263	6	US-10-498-026-31
8	69	13.5	255	6	US-10-660-499A-2
9	65.5	12.8	609	6	US-10-821-234-1611
10	65	12.7	226	6	US-10-670-009-6
11	63	12.3	614	7	US-11-052-554A-44
12	61	11.9	250	7	US-11-054-515-1460
13	61	11.9	570	7	US-11-072-512-2109
14	61	11.9	629	7	US-11-072-512-3405
15	60.5	11.8	239	7	US-11-019-711-52
16	60.5	11.8	464	6	US-10-959-322-5
17	59.5	11.6	348	7	US-11-024-959-338
18	59.5	11.6	371	6	US-10-467-657-534
19	59.5	11.6	543	7	US-11-169-041-162
20	59.5	11.6	1767	7	US-11-052-554A-372
21	58.5	11.4	165	7	US-11-098-686-10343
22	58	11.3	225	6	US-10-670-009-5
23	58	11.3	240	7	US-11-212-443-139
24	57.5	11.2	364	7	US-11-098-686-10327
25	57.5	11.2	448	7	US-11-183-205-56

26	57.5	11.2	2455	7	US-11-186-999-4	Sequence 4, Appli
27	57	11.1	495	6	US-10-770-726-81	Sequence 81, Appl
28	56.5	11.0	405	7	US-11-072-512-2176	Sequence 2176, Ap
29	56.5	11.0	601	7	US-11-072-512-2566	Sequence 2566, Ap
30	56.5	11.0	1206	6	US-10-995-561-709	Sequence 709, App
31	56.5	11.0	1307	6	US-10-995-561-711	Sequence 711, App
32	56.5	11.0	1637	6	US-10-821-234-1204	Sequence 1204, Ap
33	56.5	11.0	1905	6	US-10-877-346-44	Sequence 44, Appl
34	56.5	11.0	2256	7	US-11-144-368-4	Sequence 4, Appli
35	56.5	11.0	2458	7	US-11-186-999-6	Sequence 6, Appli
36	56.5	11.0	2458	7	US-11-186-999-13	Sequence 13, Appl
37	56.5	11.0	2483	7	US-11-186-999-2	Sequence 2, Appli
38	56	10.9	238	7	US-11-120-308-96	Sequence 96, Appl
39	56	10.9	305	7	US-11-120-308-90	Sequence 90, Appl
40	56	10.9	1252	6	US-10-493-909-89	Sequence 89, Appl
41	55.5	10.8	113	7	US-11-072-512-3153	Sequence 3153, Ap
42	55.5	10.8	240	7	US-11-212-443-177	Sequence 177, App
43	55.5	10.8	258	7	US-11-038-284-23	Sequence 23, Appl
44	55.5	10.8	356	7	US-11-212-443-56	Sequence 56, Appl
45	55.5	10.8	817	7	US-11-144-630-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-10-498-026-33
; Sequence 33, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-33

Query Match 100.0%; Score 513; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 9e-53;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TKVDLTVEKGSDAKTLVLMNIKYTRPGDTLARVELRHQSGSEWEPMTKGNLWEVKSAPL 60
Db 1 TKVDLTVEKGSDAKTLVLMNIKYTRPGDTLARVELRHQSGSEWEPMTKGNLWEVKSAPL 60
QY 61 TGPMMNFRFLSKGKMNVDDEVPTAFTVGKTYTPEYN 97
Db 61 TGPMMNFRFLSKGKMNVDDEVPTAFTVGKTYTPEYN 97

RESULT 2
US-10-498-026-32
; Sequence 32, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-32


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US-10-498-026-31
; Sequence 31, Application US/10498026
; Publication No. US2006002434A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-31

Query Match      27.8%; Score 142.5; DB 6; Length 263;
Best Local Similarity 28.7%; Pred. No. 3e-09;
Matches 27; Conservative 24; Mismatches 42; Indels 1; Gaps 1;

Qy   1 TKVDLTVKSGDAKLVLNLIKTRPGDTLAEVLRQHGSSEWEPMTK-KGNLWEVKSAKP 59
    ||| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : 
Db   168 TRPETHVERASPNYLAILKVYDGDDVAVIDKEKGDKWKIELKSNGAVWRIDTPDK 227

Qy   60 LTGPMNFRLSKGMKNVFDEVIPTFTVGKTYYT 93
    |||| | : : : : : | : : : : ~~~~~~ : : : : : 

Db   228 LAGPFVTRYTGEGTKSEPEDIPEGWKAADTSYS 261


RESULT 8
US-10-660-499A-2
; Sequence 2, Application US/10660499A
; Publication No. US20050246795A1
; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG KEUN
; APPLICANT: AHN, JI HOON
; APPLICANT: SONG, SANG KEE
; APPLICANT: CHOI, YANG DO
; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
; TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
; FILE REFERENCE: 20020-02USA
; CURRENT APPLICATION NUMBER: US/10/660,499A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: KR 2003-19069
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-660-499A-2

Query Match      13.5%; Score 69; DB 6; Length 255;
Best Local Similarity 29.6%; Pred. No. 0.97;
Matches 16; Conservative 15; Mismatches 19; Indels 4; Gaps 3;

Qy   42 WBPMTKK-GNLWEVKSAKPLTG-PNNFRLSKGMKNVFDEVIPTFTVGKTYT 93
    || : : : : : | : : : : : | : : : : : | : : : : : | : : : : : 
Db   199 WWAMSRNWSSNQ--SNAYLNQSLSFRVTTDTGETRVFDIVPVSWTFGTFS 250


RESULT 9
US-10-821-234-1611
; Sequence 1611, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1611
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1611

Query Match      12.8%; Score 65.5; DB 6; Length 609;
Best Local Similarity 27.0%; Pred. No. 7.5;
Matches 27; Conservative 16; Mismatches 38; Indels 19; Gaps 5;

Qy   2 KVLDLVFKSGDAKLVLNLIKTRPGDTLAEVELRQHGSSEWEPMTKKGNLWEVKSAKPLT 61
    |: : : : : | : : : : | : : : : | : : : : | : : : : | : : : : 
Db   451 KIMATPEQGVMKAIVEKRITFYRSDFENFLQQH-FRNLEALAL--DLMEFEQAVALDT 507

Qy   62 GP-----MNFRLSKGMKNVFDEVIPTAFTVGKTTYTPEYN 97
    ||| | : : : : : | : : : : ~~~~~~ | : : : : 

Db   508 LPKVEAMNKRL---GSLVDEFKELV-----YPDPDN 535


RESULT 10
US-10-670-009-6
; Sequence 6, Application US/10670009
; Publication No. US20050272041A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J.
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guiltinan, Mark
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Jun, Shi
; TITLE OF INVENTION: Purified Plant Expansin Proteins and DNA Encoding Same
; FILE REFERENCE: P04666US08
; CURRENT APPLICATION NUMBER: US/10/670,009
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 09/896,301
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/429,675
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 08/834,327
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 08/444,515
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: US 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: US 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-670-009-6

Query Match      12.7%; Score 65; DB 6; Length 226;
Best Local Similarity 27.1%; Pred. No. 2.4;
Matches 23; Conservative 15; Mismatches 41; Indels 6; Gaps 5;

Qy   10 GSDAKTLVLNIKTRYPRPGDTLAEVELRQHGSSEWEPMTKK-GNLWEVKSAKPLTG-PMNFR 67
    ||| | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : 
Db   141 GHSTFNLLVLTNVAGPD-VQSVSIK-GSSTGQPMSRWQNWSNSY--LDGQLSFQ 196

Qy   68 FLKSGMKNVFDEVIPTAFTVGKTY 92
```

```

US-10-498-026-31
; Sequence 31, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Lolium perenne
; US-10-498-026-31

Query Match      27.8%; Score 142.5; DB 6; Length 263;
Best Local Similarity 28.7%; Pred. No. 3e-09;
Matches 27; Conservative 24; Mismatches 42; Indels 1; Gaps 1;

Qy 1 TKVDLTVKSGDAKTLVNLNKKYTRPGDITLAELVELRQHSGSEWEPMTKK-GNLWEVKSAKP 59
||| ||| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
168 TRPETHVERKASPNYLAILKVYDGDGDDVAIDKEKGDKWKIELKSNGAVWRIDTPDK 227
||| ||| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Qy 60 LTGPNNFRLSKGMKNVFDEVIPTFTVGKTYT 93
||||| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Db 228 LTGPFTVRYTEGGTKSEPEDVIPBCKWADTSYS 261
||||| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 8
US-10-660-499A-2
; Sequence 2, Application US/10660499A
; Publication No. US20050246795A1
; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG KEUN
; APPLICANT: AHN, JI HOON
; APPLICANT: SONG, SANG KEE
; APPLICANT: CHOI, YANG DO
; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
; TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
; FILE REFERENCE: 20020-02USA
; CURRENT APPLICATION NUMBER: US/10/660,499A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: KR 2003-19069
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-660-499A-2

Query Match      13.5%; Score 69; DB 6; Length 255;
Best Local Similarity 29.6%; Pred. No. 0.97;
Matches 16; Conservative 15; Mismatches 19; Indels 4; Gaps 3;

Qy 42 WEPMTKK-GNLWEVKSAKPLTG-PNNFRLSKGMKNVFDEVIPTFTVGKTYT 93
||| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
199 WNAWSRNWGSNQ--SNAYLNQSLSFRVTDTGETRVFDIVPVSWTFGTFS 250
||| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 9
US-10-821-234-1611
; Sequence 1611, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan

```


Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3405
LENGTH: 629
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3405

Query Match 11.9%; Score 61; DB 7; Length 629;
Best Local Similarity 28.3%; Pred. No. 26;
Matches 26; Conservative 10; Mismatches 48; Indels 8; Gaps 3;
Qy 5 LTVEKGSDAKTLVNLKTRPGDTLAEVLRHGHSEWEP-----MTKGNLWEVKSAPL 60
Db 131 LLAEEWLDKKS---SEKVTREGSQYDHDSSVSENWTKYGLVAKKLTMDALSVAAV 187
Qy 61 TGPMMF-RFLSKGGMKNVDFEVIPTAFTVGKT 91
Db 188 PHSSTYVPVLDKHMVSKVDFEVPFLAHVNCNDT 219

RESULT 15
US-11-019-711-52
Sequence 52, Application US/11019711
Publication No. US20060009634A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malvankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigar, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Millier, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 239
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Laminin
OTHER INFORMATION: N-terminal domain Consensus Sequence
US-11-019-711-52

Query Match 11.8%; Score 60.5; DB 7; Length 239;
Best Local Similarity 22.1%; Pred. No. 8.6;
Matches 19; Conservative 20; Mismatches 36; Indels 11; Gaps 3;
Qy 3 VDLTVEKGSDAKTLVNLKTRPGDTLAEVLRHGHSEWEPMTKGNLWEVKSAPL 62
Db 88 VNLTLDLGKEFHLTVILKFCSPRLAILERSDFG-KTWQPYQYFSSDCRRRTFGRPRG.146
Qy 63 PMNFRFLSKGGMKNV-----FDEVIP 83
Db 147 P-----ITKGNEQEVLTSEYSDIVP 167

Search completed: February 16, 2006, 12:01:47
Job time : 18.4103 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:35 ; Search time 222.188 Seconds
(without alignments)
191.818 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVKXGSDAKTLVNI.....FDEVIPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	513	100.0	97	2	AAY25600 Lolium sp
2	513	100.0	97	7	ADC34850 Rye grass
3	513	100.0	97	8	ADJ5066 Ryegrass
4	505	98.4	97	8	ADJ5068 Ryegrass
5	433	84.4	96	8	ADJ65073 Dactylis
6	390	76.0	100	8	ADJ65077 Hordeum v
7	367	71.5	97	8	ADJ65081 Triticum
8	366	71.3	96	8	ADJ65082 Triticum
9	312.5	60.9	97	2	AAY25599 Lolium sp
10	312.5	60.9	97	7	ADC34849 Rye grass
11	307.5	59.9	96	8	ADJ65075 Lolium pe
12	292.5	57.0	96	8	ADJ65079 Phleum pr
13	292.5	57.0	122	2	AAY25614 Phleum sp
14	292.5	57.0	122	7	ADC34864 Timothy G
15	287.5	56.0	94	4	ABM00018 Allergen
16	273.5	53.3	122	2	AAR63207 Recombina
17	259.5	50.6	98	8	ADJ65078 Triticum
18	232.5	45.3	98	8	ADJ65080 Hordeum v
19	173.5	33.8	103	8	ADJ65057 Phl p 2 m
20	167.5	32.7	267	7	ABM86424 Rice abio
21	167.5	32.7	267	7	ABM90101 Rice abio
22	166.5	32.5	267	7	ABM90301 Rice abio
23	164.5	32.1	276	8	ADJ89441 Plant ful
24	154.5	30.1	253	2	AAR37921 Cyn di de

25	154	30.0	90	8	ADJ65074	Adj65074 Oryza sat
26	153.5	29.9	197	2	AAR37919	Aar37919 Cyn di de
27	153.5	29.9	197	2	AAR37920	Aar37920 Cyn di de
28	153.5	29.9	200	2	AAR37913	Aar37913 Cyn di de
29	153.5	29.9	246	6	AB880136	Abb80136 Cyn d 1 p
30	153.5	29.9	272	2	AAR37917	Aar37917 Cyn di 18
31	150.5	29.3	240	2	AAR60704	Aar60704 Dactylis
32	150.5	29.3	240	5	AAW48318	Aam48318 Orchard g
33	150.5	29.3	264	5	AAW48318	Aam48318 Orchard g
34	149.5	29.1	240	2	AAR60706	Aar60706 Phleum pr
35	149.5	29.1	263	2	AAY25612	Aay25612 Phleum sp
36	149.5	29.1	263	7	ADC34862	Adc34862 Timothy g
37	149.5	29.1	263	8	ADM12236	Adm12236 Phleum pr
38	149.5	29.1	263	8	ADO38454	Ado38454 Pollen al
39	149.5	29.1	263	8	ADQ14385	Adq14385 Timothy g
40	149.5	29.1	263	8	ADS52092	Ads52092 P pratens
41	149.5	29.1	263	8	ADS14363	Ads14363 Timothy G
42	146.5	28.6	240	2	AAR60705	Aar60705 Poa prate
43	145.5	28.4	261	2	AAR54949	Aar54949 Johnson g
44	144.5	28.2	240	5	AAU79518	Aau79518 Hypoaller
45	144.5	28.2	263	8	ADQ14384	Adq14384 Ryegrass

ALIGNMENTS

RESULT 1
AAY25600
ID AAY25600 standard; protein; 97 AA.
XX
AC AAY25600;
XX
DT 30-SEP-1999 (first entry)
XX
DE Lolium sp. allergen 126387 Lol p 3 protein fragment.
XX

XX Major histocompatibility complex; class II; desensitizing; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chitomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
OS Lolium sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-GB000080.
XX
PR 09-JAN-1998; 98GB-00000445.
XX
PR 21-SEP-1998; 98GB-00020474.
XX

(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Larche M, Kay AB;

WPI; 1999-458255/38.

Desensitizing patients to polypeptide allergens.

Example 6; Page 55; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a
CC polypeptide allergen and comprises administering to the patient a peptide
CC derived from the allergen where restriction to a MHC Class II molecule
CC possessed by the patient can be demonstrated for the peptide and the
CC peptide is able to induce a late phase response in an individual who
CC possesses the MHC Class II molecule. The methods can be used for
CC desensitizing patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chitomidae (non-biting midges), spiders and mites, housefly, fruit

CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents the Lolium sp. allergen 126385 Lol p 2a
XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 513; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.1e-54;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEEWPMTKKGNLWEVKSAPL 60
DB 1 TKVDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEEWPMTKKGNLWEVKSAPL 60
QY 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97
DB 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

RESULT 2
ADC34850
ID ADC34850 standard; protein; 97 AA.
XX
AC ADC34850;

XX 18-DEC-2003 (first entry)

XX Rye grass allergen Lol p 3.

XX rye grass; allergen; antigen; hyporesponsive; desensitisation;
KW immunomodulator; gene therapy.

XX Lolium sp.

XX WO2003047618-A2.

XX 12-JUN-2003.

XX 05-DEC-2002; 2002WO-GB005548.

XX 05-DEC-2001; 2001US-0338385P.

XX (CIRC-) CIRCASSIA LTD.

XX Larche M, Ledger PW;

XX WPI; 2003-523267/49.

XX Desensitizing an individual to a selected polypeptide antigen comprises
PT administering a composition containing polypeptide antigens in an amount
PT that generates a state of hyporesponsiveness to the antigen to allow
PT desensitization.

PS Disclosure; Page 25; 57pp; English.

XX The invention relates to a novel method for desensitising an individual
XX to a selected polypeptide antigen. The method comprises administering a
XX composition that contains polypeptide antigens in an amount that
XX generates in the individual a state of hyporesponsiveness to the antigen
XX to allow desensitisation to one or more polypeptide antigens. The method
XX of the invention has immunomodulator activity, and may have a use in gene
XX therapy. The composition and method are useful in manufacturing a
XX medicament for desensitising an individual to a selected polypeptide
XX antigen or for generating in the individual a state of hyporesponsiveness
XX to the antigen to allow desensitisation to one or more polypeptide
XX antigens. The present sequence is used in the exemplification of the
XX invention.

XX Sequence 97 AA;

Query Match 100.0%; Score 513; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.1e-54;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEEWPMTKKGNLWEVKSAPL 60
DB 1 TKVDLTVEKGSDAKTLVLNLIKTYTRPGDTLAEVELRQHGSEEWPMTKKGNLWEVKSAPL 60

QY 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97
DB 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

RESULT 3
ADJ65066
ID ADJ65066 standard; protein; 97 AA.
XX
AC ADJ65066;

XX 06-MAY-2004 (first entry)

XX Ryegrass Lol p 3 allergen protein SEQ ID NO:2.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
KW ryegrass; Lol p 3.

XX Lolium perenne.

XX WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX N-PSDB; ADJ65065.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

PS Claim 6; SEQ ID NO 2; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a polynucleotide or its conservatively modified variant having
XX a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
XX recombinant expression cassette (II) comprising (1); (2) a vector (III)
XX comprising (II); (3) a host cell comprising (III); (4) a group 2/3
XX allergen encoding a polypeptide comprising any of the 12 sequences of 90-
XX 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
XX ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
XX (6) an antibody that selectively binds to (IV); (7) a method of modifying
XX cell walls in the tissues of a transgenic plant, comprising introducing
XX into a plant an expression cassette comprising a promoter active in cells
XX of plants operably linked to a group 2/3 allergen polynucleotide which
XX specifically hybridises to S1 under stringent conditions; (8) a method for
XX weakening the mechanical strength of cellulose fibres; (9) a method for
XX producing a polypeptide having expansin activity; (10) a transgenic plant
XX cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
XX with a genome comprising a nucleic acid that comprises S1 and that
XX possesses expansin activity, or a transgenic plant comprising an
XX expression cassette operably linked to a group 2/3 allergen
XX polynucleotide which specifically hybridises to S1 under stringent
XX conditions; and (12) seeds of the plant described above, which carry the

CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents the ryegrass
 CC Lol p 3 allergen, which is used in the exemplification of the present
 CC invention.

XX Sequence 97 AA;

Query Match 100.0%; Score 513; DB 8; Length 97;
 Best Local Similarity 100.0%; Pred. No. 6.1e-54; Indels 0; Gaps 0;
 Matches 97; Conservative 0; Mismatches 0;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
 Db 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60

QY 61 TGPMMFRLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97
 Db 61 TGPMMFRLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

RESULT 4

ADJ65068
 ID ADJ65068 standard; protein; 97 AA.

AC ADJ65068;

DT 06-MAY-2004 (first entry)

DE Ryegrass Lol p 3 allergen modified variant protein SEQ ID NO:4.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
 KW ryegrass; Lol p 3; modified; variant.

OS Lolium perenne.
 OS Synthetic.

XX WO2004011025-A1.

PD 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX Disclosure; SEQ ID NO 4; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
 CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which

CC specifically hybridises to S1 under stringent conditions; (8) a method of
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents a modified
 CC variant ryegrass Lol p 3 allergen protein sequence, which is used in the
 CC exemplification of the present invention.

XX Sequence 97 AA;

Query Match 98.4%; Score 505; DB 8; Length 97;
 Best Local Similarity 99.0%; Pred. No. 5.7e-53; Indels 0; Gaps 0;
 Matches 96; Conservative 0; Mismatches 1;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
 Db 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60

QY 61 TGPMMFRLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

Db 61 TGPMMFRLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

RESULT 5

ADJ65073
 ID ADJ65073 standard; protein; 96 AA.

XX AC ADJ65073;

XX 06-MAY-2004 (first entry)

XX Dactylis glomerata allergen amino acid sequence SEQ ID NO:9.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX Dactylis glomerata.

XX WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX Claim 6; SEQ ID NO 9; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3

CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX SQ Sequence 96 AA;
Query Match 84.4%; Score 433; DB 8; Length 96;
Best Local Similarity 85.1%; Pred. No. 3e-44;
Matches 80; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 KVDLTVEKGSDAKTLVNLKITYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 61
DB 2 KVTFFVEKGSDDPKVLVDIKITYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 61
OY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
DB 62 GPFNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95

RESULT 6
ADJ65077
ID ADJ65077 standard; protein; 100 AA.
XX AC ADJ65077;
XX DT 06-MAY-2004 (first entry)
XX DE Hordeum vulgare allergen amino acid sequence SEQ ID NO:13.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.
XX OS Hordeum vulgare.
XX PN WO2004011025-A1.
XX PD 05-FEB-2004.
XX PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX WPI; 2004-143737/14.
XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.
XX Claim 6; SEQ ID NO 13; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 231 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (1); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX SQ Sequence 100 AA;

Query Match 76.0%; Score 390; DB 8; Length 100;
Best Local Similarity 74.2%; Pred. No. 5.2e-39;
Matches 72; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
OY 1 TKVDLTVEKGSDAKTLVNLKITYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
DB 3 TKVKFTVQKGSDAKKLVLDKIDYTRAGDTLSMELRQHGSEWEPMTKGDMWELSSKPL 62
OY 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
DB 63 VGPFNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYVD 99

RESULT 7
ADJ65081
ID ADJ65081 standard; protein; 97 AA.
XX AC ADJ65081;
XX DT 06-MAY-2004 (first entry)
XX DE Triticum aestivum allergen amino acid sequence SEQ ID NO:17.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.
XX OS Triticum aestivum.
XX PN WO2004011025-A1.
XX PD 05-FEB-2004.
XX PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX WPI; 2004-143737/14.

PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

PS Claim 6; SEQ ID NO 17; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 97 AA;

Query Match 71.5%; Score 367; DB 8; Length 97;
Best Local Similarity 70.5%; Pred. No. 3e-36;
Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Oy 2 KVDLTVEKGSDAKTLVLNLIKTRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPLPT 61
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
3 RVKLTVEKGSDDKKLALKIDYTRPNDLSLSEVELRQHGSEWEPMTKGNLWEVKSAPLPT 62

Oy 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGTQYTPY 96

Db 63 GPFNFRFLSKGGMKNVDFEVIPTAFTVGTQYTPY 97

RESULT 8

ADJ65082
ID ADJ65082 standard; protein; 96 AA.

XX ADJ65082;

XX 06-MAY-2004 (first entry)

DE Triticum aestivum allergen amino acid sequence SEQ ID NO:18.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX Triticum aestivum.

XX WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX

PA (PENN-) PENN STATE RES FOUND.

PI Li L, Cosgrove D;

DR WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

PS Claim 6; SEQ ID NO 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

Query Match 71.3%; Score 366; DB 8; Length 96;
Best Local Similarity 70.5%; Pred. No. 4e-36;
Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Oy 2 KVDLTVEKGSDAKTLVLNLIKTRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPLPT 61
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
2 KVKLTVEKGSDDKKLALKIDYTRPNDLSLSEVELRQHGSEWEPMTKGNLWEVKSAPLPT 61

Oy 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGTQYTPY 96

Db 62 GPFNFRFLSKGGMKNVDFEVIPTAFTVGTQYTPY 96

RESULT 9

AAJ25599
ID AAJ25599 standard; protein; 97 AA.

XX AAJ25599;

XX 30-SEP-1999 (first entry)

DE Lolium sp. allergen 126386 Lol p 2a protein fragment.

XX Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

OS	Lolium sp.
PN	WO9934826-A1.
XX	
PD	15-JUL-1999.
XX	
PP	11-JAN-1999; 99WO-GB0000080.
XX	
PR	09-JAN-1998; 98GB-00000445.
PR	21-SEP-1998; 98GB-00020474.
XX	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA	
XX	Larche M, Kay AB;
PI	
PT	WPI; 1999-458255/39.
DR	
XX	Desensitizing patients to polypeptide allergens.
PS	Example 6; Page 55; 117pp; English.
XX	This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents the Lolium sp. allergen 126385 Lol p 2a
XX	
SQ	Sequence 97 AA;
	Query Match 60.9%; Score 312.5; DB 2; Length 97;
	Best Local Similarity 60.6%; Pred. No. 1.2e-29;
	Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;
Qy	3 VDLTVKSGDAKTIVLNKYTRPGDTLAEVELROHGSSEWEPMTKGN-LWEVKSAPLT 61 ::: ::: ::: ::: ::: ::: :::
Db	4 VEFTVEKGSDEKNLSIKYKNGGSMVAELKEHGSGNEWLAKKGDCGVWEIKSDPLK 63 ::: ::: ::: ::: ::: ::: :::
Qy	62 GPMNFRFLSKGMKNVFDEVIPITFTVGKTYTPE 95 :: ::
Db	64 GPFFNRFVSEKGRNVFDDVVPADEFKVGTYYKPE 97
RESULT 10	
ADC34849	
ID	ADC34849 standard; protein; 97 AA.
XX	
AC	ADC34849;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Rye grass allergen Lol p 2a.
XX	
KW	rye grass; allergen; antigen; hyporesponsive; desensitisation;
KW	immunomodulator; gene therapy.
XX	
OS	Lolium sp.
XX	
PN	WO2003047618-A2.
XX	
PD	12-JUN-2003.
XX	
PF	05-DEC-2002; 2002WO-GB005548.

PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 11; 73pp; English.

PS The present invention describes an isolated nucleic acid molecule (I)
XX comprising a polynucleotide or its conservatively modified variant having
XX a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

Query Match 59.9%; Score 307.5; DB 8; Length 96;
Best Local Similarity 60.2%; Pred. No. 4.9e-29;
Matches 56; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Qy 3 VDLTVKSGDAKTLVLNLIKTRPGDTLAEVLHQHSGSEWEPMTKGN-LWEVKSAPL 61
Db 4 VEFTVEKSGDEKLNALS1KYNKEGDSMAEVELKEHGSNEWLALKKNGDGVWEIKSDKPLK 63

Qy 62 GPMNFRFLSKGKMNVPFDEVPTAFTVGKTYTP 94

Db 64 GPFNFRFVSEKGMNVFDDVVPADPKVGTITYP 96

RESULT 12

ADJ65079

ID ADJ65079 standard; protein; 96 AA.

XX ADJ65079;

XX 06-MAY-2004 (first entry)

XX Phleum pratense allergen amino acid sequence SEQ ID NO:15.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX Phleum pratense.

XX WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX

(PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 15; 73pp; English.

CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method for
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

Query Match 57.0%; Score 292.5; DB 8; Length 96;
Best Local Similarity 58.9%; Pred. No. 3.2e-27;

Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

Qy 2 KVDLTVKSGDAKTLVLNLIKTRPGDTLAEVLHQHSGSEWEPMTK-KGNLWEVKSAPL 60

Db 3 KVTFTVEKSGNEKHLAVLVKY--EGDTMAEVELKEHGSDEWVAMTKGSGVMTFDSBPPL 60

Qy 61 TGMNFRFLSKGKMNVPFDEVPTAFTVGKTYTP 95

Db 61 QGPFNFRPLTEKGMNVFDDVVPKTYTIGATYAP 95

RESULT 13

AAAY25614

ID AAAY25614 standard; protein; 122 AA.

XX AAAY25614;

XX 30-SEP-1999 (first entry)

XX Phleum sp. allergen Phl p 2 protein fragment #1.

XX Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

OS	Phleum sp.	XX
XX	WO9934826-A1.	XX
XX	15-JUL-1999.	XX
PD	11-JAN-1999; 99WO-GB000080.	XX
XX	09-JAN-1998; 98GB-00000445.	XX
XX	21-SEP-1998; 98GB-00020474.	XX
XX	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.	XX
XX	Larche M, Kay AB;	XX
XX	WPI; 1999-458255/38.	XX
DR	Desensitizing patients to polypeptide allergens.	XX
PT	Example 6; Page 59; 117pp; English.	XX
XX	This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 2 allergen	XX
XX	Sequence 122 AA;	XX
SQ	Query Match 57.0%; Score 292.5; DB 2; Length 122; Best Local Similarity 58.9%; Pred. No. 4.4e-27; Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;	XX
Qy	2 KVDLTVEKGSDAKTLVNIKYTRPGDTLAEVLRQHSSEWEPMTK-KGNLWEVKSAPL 60	XX
Db	29 KVTFTVEKGSNEKHLAVLVKY--EGDTMAEVELRHSDEWVANTKGGGVWTFDSEPL 86	XX
Qy	61 TGPMPNFRFLSKGKMNVDDEVIPFTVGTGKTYTPE 95	XX
Db	87 QGPFNFRFLTEKGMKNVDFDDVPEKTYTGATYAPE 121	XX
RESULT 14		XX
AD34864		XX
ID	AD34864 standard; protein; 122 AA.	XX
AC	AD34864;	XX
XX	18-DEC-2003 (first entry)	XX
DT	Timothy grass allergen Phl p 2.	XX
DE	allergen; antigen; hyporesponsive; desensitisation; immunomodulator;	XX
XX	gene therapy; timothy grass.	XX
KW	Phleum sp.	XX
OS	WO2003047618-A2.	XX
XX	12-JUN-2003.	XX
PD	05-DEC-2002; 2002WO-GB005548.	XX
XX		XX
PF		XX

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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:55:30 ; Search time 55.547 Seconds
(without alignments)
144.374 Million cell updates/sec

Title: US-10-628-296A-2
Perfect score: 513
Sequence: 1 TKVDLTVKSGDAKTLVNLNI.....FDEVIPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.5	30.1	246	US-08-441-507-21	Sequence 21, Appl
2	154.5	30.1	246	US-07-969-875A-21	Sequence 21, Appl
3	153.5	29.9	197	US-08-441-507-5	Sequence 5, Appl
4	153.5	29.9	197	US-07-969-875A-5	Sequence 5, Appl
5	153.5	29.9	200	US-08-441-507-4	Sequence 4, Appl
6	153.5	29.9	200	US-07-969-875A-4	Sequence 4, Appl
7	153.5	29.9	272	US-08-441-507-15	Sequence 15, Appl
8	153.5	29.9	272	US-07-969-875A-15	Sequence 15, Appl
9	149.5	29.1	263	US-09-811-672-10	Sequence 10, Appl
10	149	29.0	30	US-08-433-854-9	Sequence 9, Appl
11	149	29.0	30	US-08-174-745A-9	Sequence 9, Appl
12	149	29.0	30	US-08-195-947-9	Sequence 9, Appl
13	149	29.0	30	US-08-433-885-9	Sequence 9, Appl
14	149	29.0	30	US-08-433-908B-9	Sequence 9, Appl
15	149	29.0	30	US-08-410-614-9	Sequence 9, Appl
16	149	29.0	31	US-08-413-974-25	Sequence 25, Appl
17	149	29.0	31	US-08-434-18-25	Sequence 25, Appl
18	149	29.0	31	US-08-433-288-25	Sequence 25, Appl
19	149	29.0	31	US-08-174-739A-25	Sequence 25, Appl
20	149	29.0	31	US-08-434-256-25	Sequence 25, Appl
21	145.5	28.4	261	US-07-971-096-2	Sequence 2, Appl
22	145.5	28.4	261	US-08-175-096-2	Sequence 2, Appl
23	142.5	27.8	263	US-09-071-252-19	Sequence 19, Appl
24	141.5	27.6	145	US-08-413-974-4	Sequence 4, Appl
25	141.5	27.6	145	US-08-434-418-4	Sequence 4, Appl
26	141.5	27.6	145	US-08-433-288-4	Sequence 4, Appl
27	141.5	27.6	145	US-08-174-739A-4	Sequence 4, Appl

28	141.5	27.6	145	2	US-08-434-256-4	Sequence 4, Appl
29	140.5	27.4	145	2	US-08-441-507-2	Sequence 2, Appl
30	140.5	27.4	145	2	US-07-969-875A-2	Sequence 2, Appl
31	137.5	26.8	138	2	US-08-441-507-7	Sequence 7, Appl
32	137.5	26.8	138	2	US-07-969-875A-7	Sequence 7, Appl
33	135.5	26.4	263	1	US-07-971-096-4	Sequence 4, Appl
34	135.5	26.4	263	1	US-08-175-096-4	Sequence 4, Appl
35	135.5	26.4	263	2	US-08-413-974-6	Sequence 6, Appl
36	135.5	26.4	263	2	US-08-434-418-6	Sequence 6, Appl
37	135.5	26.4	263	2	US-08-433-288-6	Sequence 6, Appl
38	135.5	26.4	263	2	US-08-174-739A-6	Sequence 6, Appl
39	135.5	26.4	263	2	US-08-434-256-6	Sequence 6, Appl
40	127.5	24.9	145	2	US-08-441-507-16	Sequence 16, Appl
41	127.5	24.9	145	2	US-07-969-875A-16	Sequence 16, Appl
42	127.5	24.9	245	2	US-08-441-507-24	Sequence 24, Appl
43	127.5	24.9	245	2	US-07-969-875A-24	Sequence 24, Appl
44	126.5	24.7	269	2	US-09-071-252-18	Sequence 18, Appl
45	124.5	24.3	86	2	US-08-441-507-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-441-507-21
; Sequence 21, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; NUMBER OF INVENTION: Dactylon
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-507-21

Query Match 30.1%; Score 154.5; DB 2; Length 246;
Best Local Similarity 35.1%; Pred. No. 1.1e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;
QY 1 TKVDLTVKSGDAKTLVNLNIKYTRPGDTLAEVLRHQSGSEWEPMTKK-GNLWEVKSARP 59

Db 146 TKITFHIEKSGNDHLYALLVKYAGDGNIVADIKPRDSDEFIPMKSSWGAIWRIDPKKP 205
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 206 LKGPFSIRLTSEGGAHLVQDDVIPANWKPDVTYT 239

RESULT 2

US-07-969-875A-21
; Sequence 21, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.;
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-969-875A-21

Query Match 30.1%; Score 154.5; DB 2; Length 246;
Best Local Similarity 35.1%; Pred. No. 1.1e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;
QY 1 TKVDLTVEKSGDAKTLVNIKYTRPGDTLAEVLHQHSGEWEPMTKK-GNLWEVKSACP 59
Db 146 TKITFHIEKSGNDHLYALLVKYAGDGNIVADIKPRDSDEFIPMKSSWGAIWRIDPKKP 205
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 206 LKGPFSIRLTSEGGAHLVQDDVIPANWKPDVTYT 239

RESULT 3

US-08-441-507-5
; Sequence 5, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon

; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-441-507-5

Query Match 29.9%; Score 153.5; DB 2; Length 197;
Best Local Similarity 35.1%; Pred. No. 1.1e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;
QY 1 TKVDLTVEKSGDAKTLVNIKYTRPGDTLAEVLHQHSGEWEPMTKK-GNLWEVKSACP 59
Db 99 TKITFHIEKSGNDHLYALLVKYAGDGNIVADIKPRDSDEFIPMKSSWGAIWRIDPKKP 158
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 159 LKGPFSIRLTSEGGAHLVQDDVIPANWKPDVTYT 192

RESULT 4

US-07-969-875A-5
; Sequence 5, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:

US-08-441-507-15
; Sequence 15, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5-8
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15-16
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 71-72
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
US-08-441-507-15
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Best Local Similarity 35.1%; Pred. No. 1.8e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;
QY 1 TKVDLTVEKSGDAKTLVLNINIKYTRPGDTLAEVELRQHGSEWEPMYTKK-GNLWEVKSAXP 59
DB 172 TKITFHIEKSDNHYLALLVKAAGDGNIVAVDIKPKDSDEFTIPMKSSWGAIWRIDPKKP 231

US-07-969-875A-15
; Sequence 15, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A..
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5-8
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15-16
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 71-72
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
US-07-969-875A-15
Query Match 29.9%; Score 153.5; DB 2; Length 272;
Best Local Similarity 35.1%; Pred. No. 1.8e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;
QY 1 TKVDLTVEKSGDAKTLVLNINIKYTRPGDTLAEVELRQHGSEWEPMYTKK-GNLWEVKSAXP 59
DB 172 TKITFHIEKSDNHYLALLVKAAGDGNIVAVDIKPKDSDEFTIPMKSSWGAIWRIDPKKP 231

QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGVKTYT 93
DB 232 LKGFPSIRLTSEGGAHLVQDDVIPANWKPDVTYT 265

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Db 172 TKITTHIEKSGNDHYLALLVKYAAAGDNIVADIKPKDSDEFIPKSSWGAIWRIDPKKP 231
Qy 60 LTGPMNFRFLSKGGMKNVDEVIPTAFTVGKTY 93
Db 232 LAGPFSIRLTSEGAHLVQDDVIPANWKPDVTYT 265

RESULT 9
US-09-811-672-10
; Sequence 10, Application US/09811672
; Patent No. 6559120
; GENERAL INFORMATION:
; APPLICANT: BALL, Tanja
; APPLICANT: VRTALA, Susanne
; APPLICANT: SPERR, Wolfgang
; APPLICANT: VALENT, Peter
; APPLICANT: SUSANI, Markus
; APPLICANT: KRAFT, Dietrich
; APPLICANT: VALENTA, Rudolf
; APPLICANT: LAFFER, Sylvia
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT
; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGN
; TITLE OF INVENTION: THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
; FILE REFERENCE: 1614-0247P
; CURRENT APPLICATION NUMBER: US/09/811,672
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Timothy Grass
US-09-811-672-10

Query Match 29.1%; Score 149.5; DB 2; Length 263;
Best Local Similarity 31.2%; Pred. No. 5.6e-11;
Matches 29; Conservative 21; Mismatches 42; Indels 1; Gaps 1;

Qy 1 TKVDLTVEKSGDAKTLVLNLIKVTGPGDTLAEVLQHGSEWEPMTKK-GNLWEVKSAKP 59
Db 168 TKVTHVEKSGNPYVALLVKYVNGDGVADVIEKKGDKWIELKESWGAIWRIDTPDK 227

Qy 60 LTGPMNFRFLSKGGMKNVDEVIPTAFTVGKTY 92
Db 228 LTGPFTVAVTTEGGTKTEAEDVIPGKADTSY 260

RESULT 10
US-08-433-854-9
; Sequence 9, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-9

Query Match 29.0%; Score 149; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKSGDAKTLVLNLIKVTGPGDTLA 30
Db 1 TKVDLTVEKSGDAKTLVLNLIKVTGPGDTLA 30

RESULT 11
US-08-174-745A-9
; Sequence 9, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
```



```

CORRESPONDENCE ADDRESS:
ADDRESS: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,908B
FILING DATE: 02-MAY-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-908B-9

Query Match          29.0%; Score 149; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30
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Db      1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30

RESULT 15
US-08-410-614-9
; Sequence 9, Application US/08410614
; Patent No. 6277383
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ongi, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/195,947
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; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-410-614-9

Query Match          29.0%; Score 149; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30
      |||||
Db      1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30

Search completed: February 16, 2006, 11:57:17
Job time : 56.547 secs
```

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:40 ; Search time 50.2564 Seconds
(without alignments)
280.771 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95

Sequence: 1 TKVDLTVKSGDAKTLVLNI 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	95	100.0	97	1	MPAL3_LOLPR	P14948 lolium pere
2	95	100.0	97	2	Q540P9_LOLPR	Q540p9 lolium pere
3	59	62.1	118	1	Q41576_WHEAT	Q41576 triticum ae
4	58	61.1	97	1	MPAL2_LOLPR	P14947 lolium pere
5	57	60.0	96	1	MPAG3_DACGL	P93124 dactylis gl
6	56	58.9	97	2	Q69B42_PHLPR	Q69B42 phleum prat
7	55	57.9	36	1	MPAG2_DACGL	Q41183 dactylis gl
8	54	56.8	88	2	Q40239_LOLPR	Q40239 lolium pere
9	50	52.6	333	2	Q5KWR0_GEOKA	Q5Kwr0 geobacillus
10	50	52.6	356	1	RUVB_PROMA	Q7v9q4 prochloroco
11	49.5	52.1	837	2	Q81HR4_PLAF7	Q81hr4 plasmodium
12	49.5	52.1	837	2	Q9BJC6_PLAFA	Q9bjc6 plasmodium
13	49	51.6	352	1	RUVB_PROMM	Q7w910 prochloroco
14	48	50.5	292	2	Q4H1F6_9STRE	Q4h1f6 streptococc
15	48	50.5	336	2	Q9CDH4_LACLA	Q9cdh4 lactococcus
16	48	50.5	531	2	Q5APJ6_CANAL	Q5apj6 candida alb
17	47	49.5	320	2	Q915X6_STFGN	Q915x6 streptococc
18	47	49.5	336	2	Q68A23_STFGN	Q68a23 streptococc
19	47	49.5	348	1	RUVB_SYNFX	Q7u9w7 synecococc
20	47	49.5	611	2	Q9VSS1_DROME	Q9vss1 drosophila
21	47	49.5	685	1	PKN2_GLOPE	Q8xj18 clostridium
22	46.5	48.9	402	2	Q7R7E0_PLAYO	Q7r7e0 plasmodium
23	46.5	48.9	762	2	Q7RRK5_PLAYO	Q7rrk5 plasmodium
24	46.5	48.9	796	2	Q4XX68_PLACH	Q4xx68 plasmodium
25	46.5	48.9	808	2	Q4YR00_PLABE	Q4yrr0 plasmodium
26	46.5	48.9	811	2	Q8WR18_PLAYO	Q8wr18 plasmodium
27	46	48.4	323	2	Q6C177_YARLI	Q6cl177 yarowia li
28	46	48.4	631	2	Q72PA5_LEPIC	Q72pa5 leptospira
29	46	48.4	631	2	Q8F742_LEPIN	Q8f742 leptospira
30	46	48.4	723	2	Q5ZLC2_CHICK	Q5zlc2 gallus gall
31	46	48.4	2621	2	Q91LMZ3_ARATH	Q91lmz3 arabidopsis

32	46	48.4	2658	2	Q9SGE4_ARATH	Q9sgE4 arabidopsis
33	45	47.4	122	1	MPAP2_PHLPR	P43214 phleum prat
34	45	47.4	122	2	Q712N1_POAL	Q712n1 lolium ital
35	45	47.4	122	2	Q712N2_WHEAT	Q712n2 triticum ae
36	45	47.4	122	2	Q712N3_POAPR	Q712n3 poa pratens
37	45	47.4	122	2	Q712N4_HOLIA	Q712n4 holcus lana
38	45	47.4	122	2	Q9ZRU0_CYNDA	Q9zru0 cynodon dac
39	45	47.4	122	2	Q9ZRU1_DACGL	Q9zru1 dactylis gl
40	45	47.4	208	2	Q4S3C2_TETNG	Q4s3c2 tetraodon n
41	45	47.4	336	2	Q8VVB9_STRTG	Q8vvb9 streptococc
42	45	47.4	345	2	Q5LY22_STRT1	Q5ly22 streptococc
43	45	47.4	345	2	Q5M2M7_STRT2	Q5m2m7 streptococc
44	45	47.4	561	2	Q4WN01_ASPFU	Q4wn01 aspergillus
45	44	46.3	126	2	Q37981_BPA51	Q37981 bacterioph

ALIGNMENTS

RESULT 1

MPAL3_LOLPR

ID MPAL3_LOLPR STANDARD; PRT; 97 AA.
AC P14948;
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Pollen allergen Lol p 3 (Lol p III).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90105394; PubMed=2605214;
RA Ansari A.A., Shenbagamurthi P., Marsh D.G.;
RT "Complete primary structure of a Lolium perenne (perennial rye grass)
RT pollen allergen, Lol p III: comparison with known Lol p I and II
RT sequences.";
RL Biochemistry 28:8665-8670(1989).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
CC pollen allergy. Binds to IgE.
CC -!- SIMILARITY: Belongs to the expansin family.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR: A33422; A33422.
CC HSP: P43214; 1WHO.
CC Gramene: P14948; -.
CC InterPro: IPR005453; Allergen Lolp2.
CC InterPro: IPR007117; Expan_Lol_p1.C.
CC Pfam: PF01357; Pollen_allerg_1.
CC PRINTS: PR01637; LOLP2ALLERGN.
CC PROSITE: PS50843; EXPANSIN_CBD; 1.
CC Allergen; Direct protein sequencing; Multigene family.
CC DOMAIN 14 94 Expansin-like CBD.
CC VARIANT 6 6 T -> M.
CC SEQUENCE 97 AA; 10907 MW; ABBAED2D6F20D24 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVKSGDAKTLVLNI 20

Db 1 TKVDLTVKSGDAKTLVLNI 20

RESULT 2	
Q540P9_LOLPR	PRELIMINARY; PRT; 97 AA.
AC Q540P9;	
DT 13-SEP-2005 (TREMBlrel. 31, Created)	
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)	
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)	
DE Grass pollen allergen Lol p 3 (Fragment).	
OS Lolium perenne (Perennial ryegrass).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	
OC Poaceae; Lolium.	
OC NCBI_TaxID=4522;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Li L.-C., Shieh M.W., Cosgrove D.J.;	
RT "Group 2 and group 3 allergens of grass pollen have plant cell wall-	
RT loosening activity characteristic of beta-expansins.";	
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AY135645; AAN12883.1; -; Genomic_DNA.	
FT NON_TER 1	
FT NON_TER 97	
SQ SEQUENCE 97 AA; 10907 MW; ABBAED2D6F20D24 CRC64;	
Query Match 100.0%; Score 95; DB 2; Length 97;	
Best Local Similarity 100.0%; Pred. NO. 7.3e-08;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 TKVDLTVEKGSDAKTLVLNI 20	
Db 1 TKVDLTVEKGSDAKTLVLNI 20	
RESULT 3	
Q41576 WHEAT	PRELIMINARY; PRT; 118 AA.
AC Q41576;	
DT 01-NOV-1996 (TREMBlrel. 01, Created)	
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)	
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)	
DE Pollen allergen-like protein.	
GN Name=Tri a III;	
OS Triticum aestivum (Wheat).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	
OC Triticeae; Triticum.	
OC NCBI_TaxID=4565;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Balzer H.J., Borysiuk L., Meyer H., Matzk F., Baumlein H.;	
RT "A pollen allergen encoding gene is expressed in wheat ovaries.";	
RL Plant J. 0:0-0(0).	
RN [2]	
RP NUCLEOTIDE SEQUENCE.	
RA Balzer H.J.;	
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.	
DR EMBL; Z50867; CAA90746.1; -; mRNA.	
DR PIR; T06550; T06550.	
DR HSP; P43214; IWHO.	
DR GO; GO:0005576; C:extracellular region; IEA.	
DR InterPro; IPR005453; Allergen Lolp2.	
DR Pfam; PF01357; Pollen allerg 1; 1.	
DR PRINTS; PRO1637; LOLP2ALLERGN.	
DR PROSITE; PS50843; EXPANSIN CBD; 1.	
SQ SEQUENCE 118 AA; 13262 MW; 76EA78BA219A8587 CRC64;	
Query Match 62.1%; Score 59; DB 2; Length 118;	
Best Local Similarity 68.4%; Pred. NO. 0.11;	
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	
Qy 3 VDLTVEKGSDAKTLVLNI 20	
Db 4 VFTVEKGSDEKNLALS 21	
RESULT 5	
MPAG3_DACGL	STANDARD; PRT; 96 AA.
ID MPAG3_DACGL	
AC P93124;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 10-MAY-2005 (Rel. 47, Last annotation update)	
DE Pollen allergen Dac g 3 (Dac g III) (Fragment).	
OS Dactylis glomerata (Orchard grass) (Cock's-foot grass).	
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Dactylis.
 OC NCBI_TaxID=4509;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP TISSUE=Pollen;
 RC MEDLINE=96406988; PubMed=8811075; DOI=10.1016/0161-5890(96)00015-6;
 RA Guerin-Marchand C., Senechal H., Bouin A.P., Leduc-Brodard V.,
 RA Taudou G., Weyer A., Peltre G., David B.;
 RT "Cloning, sequencing and immunological characterization of Dac g 3, a
 RT major allergen from Dactylis glomerata pollen.";
 RL Mol. Immunol. 33:797-806(1996).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
 CC pollen allergy. Binds to IgE.
 CC -!- SIMILARITY: Belongs to the expansin family.
 CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U25343; AAB42200.1; -; mRNA.
 DR HSSP; P43214; 1WHO.
 DR InterPro; IPR005453; Allergen Lolp2.
 DR InterPro; IPR007117; Expan_Lol_p1_C.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01637; LOLLP2ALLERGN.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 KW Allergen.
 FT DOMAIN 14 94 Expansin-like CBD.
 FT NON_TER 1 1
 FT SEQUENCE 96 AA; 10933 MW; 9DF6B5965405A925 CRC64;
 SQ
 Query Match 60.0%; Score 57; DB 1; Length 96;
 Best Local Similarity 68.4%; Pred. No. 0.19;
 Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 2 KVDLTVKSGSDAKTLVLNI 20
 DB 2 KVTFTVKSGSDPKGLVLDI 20
 RESULT 6
 Q69B42_PHLPR PRELIMINARY; PRT; 97 AA.
 ID Q69B42_PHLPR PRELIMINARY; PRT; 97 AA.
 AC Q69B42;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phl p 3 allergen (Fragment).
 OS Phleum pratense (Common timothy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Avenae; Phleum.
 OC NCBI_TaxID=15957;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Petersen A., Suck R., Cromwell O., Becker W.M.;
 RT "Cloning, expression and characterization of the grass pollen allergen
 RT Phl p 3".
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A421969; AAR31142.1; -; Genomic DNA.
 DR GO; GO:0005576; C:extracellular region; TRA.
 DR InterPro; IPR005453; Allergen Lolp2.
 DR InterPro; IPR007117; Expan_Lol_p1_C.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01637; LOLLP2ALLERGN.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 FT NON_TER 1 1
 FT SEQUENCE 97 AA; 10959 MW; CD2E56B0C1B65156 CRC64;
 SQ

Query Match 58.9%; Score 56; DB 2; Length 97;
 Best Local Similarity 63.2%; Pred. No. 0.29;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 2 KVDLTVKSGSDAKTLVLNI 20
 DB 3 QVFTTVKSGSDPKGLVLDI 21
 RESULT 7
 MPAG2_DACGL STANDARD; PRT; 36 AA.
 ID MPAG2_DACGL STANDARD; PRT; 36 AA.
 AC Q41183;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Pollen allergen Dac g 2 (Dac g II) (Fragment).
 OS Dactylis glomerata (Orchard grass) (Cock s-foot grass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Dactylis.
 OC NCBI_TaxID=4509;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92406239; PubMed=1526648;
 RA Roberts A.M., van Ree R., Cardy S.M., Bevan L.J., Walker M.R.;
 RT "Recombinant pollen allergens from Dactylis glomerata: preliminary
 RT evidence that human IgE cross-reactivity between Dac g II and Lol p
 RT I/II is increased following grass pollen immunotherapy.";
 RL Immunology 76:389-396(1992).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
 CC pollen allergy. Binds to IgE.
 CC -!- SIMILARITY: Belongs to the expansin family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; S45354; AAB23303.1; ALT_TERM; mRNA.
 DR HSSP; P43214; 1WHO.
 DR InterPro; IPR007117; Expan_Lol_p1_C.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 KW Allergen.
 FT NON_TER 1 1
 FT NON_TER 36 36
 FT SEQUENCE 36 AA; 3971 MW; B7FFB416DD0B0852 CRC64;
 SQ
 Query Match 57.9%; Score 55; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 0.14;
 Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 3 VDLTVKSGSDAKTLVLNI 20
 DB 4 VTFTVKSGSDPKGLVLDI 21
 RESULT 8
 Q40239_LOLPR PRELIMINARY; PRT; 88 AA.
 ID Q40239_LOLPR PRELIMINARY; PRT; 88 AA.
 AC Q40239;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Allergen Lol p II (Fragment).
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Lolium.
 OC NCBI_TaxID=4522;
 RN [1]

DR TIGRFAMs; TIGR00635; ruvB; 1.
 SW Complete proteome; Helicase.
 KQ SEQUENCE 333 AA; 36754 MW; 9CE23DC0219A7184 CRC64;

Query Match 52.6%; Score 50; DB 2; Length 333;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 VDLTVEKSGDAKTLVLNI 20
 :||: || ||: ||: ||:
 Db 133 LDIITICKGPDARTLRDL 150

RESULT 10
 RUVB_PROMA STANDARD; PRT; 356 AA.
 ID RUVB_PROMA AC Q7V9Q4;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holliday junction DNA helicase ruvB.
 GN Name=ruvB; OrderedLocusNames=Prol775;
 OS Prochlorococcus marinus.
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
 OC Prochlorococcus.
 CC Prochlorococcus.
 CC NCBI_TaxID=1219;
 RN [1]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=SARG / CCMP 1375 / SS120;
 RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
 RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
 RA Makarova K.S., Ostrowski K.M., Oztas S., Robert C., Rogozin I.B.,
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
 RA Wolf Y.I., Hess W.R.;
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
 RT a nearly minimal oxyphototrophic genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
 CC -1- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures
 CC cruciform structure in supercoiled DNA with palindromic sequence,
 CC indicating that it may promote strand exchange reactions in
 CC homologous recombination. RuvAB is an helicase that mediates the
 CC Holliday junction migration by localized denaturation and
 CC reannealing (By similarity).
 CC -1- SUBUNIT: Forms a complex with ruvA (By similarity).
 CC -1- SIMILARITY: Belongs to the ruvB family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AB017166; AAQ00819.1; -; Genomic_DNA.
 CC HAMAP; MF 00016; -; 1.
 CC InterPro; IPR003593; AAA_ATPase.
 CC InterPro; IPR003959; AAA_ATPase_cent.
 CC InterPro; IPR004605; RuvB.
 CC InterPro; IPR008823; RuvB_C.
 CC InterPro; IPR008824; RuvB_N.
 CC InterPro; IPR011991; Wing_hlx_DNA_bd.
 CC Pfam; PF00004; AAA; 1.
 CC Pfam; PF05491; RuvB_C; 1.
 CC Pfam; PF05496; RuvB_N; 1.
 CC SMART; SM00382; AAA; 1.
 CC TIGRFAMs; TIGR00635; ruvB; 1.
 CC ATP-binding; Complete proteome; DNA damage; DNA recombination;
 CC DNA repair; Helicase; Hydrolyase; Nucleotide-binding; SOS response.
 FT NP_BIND 79 86
 QY SEQUENCE 356 AA; 39305 MW; C9BA758303A1396A CRC64;

Query Match 52.6%; Score 50; DB 1; Length 356;
 Best Local Similarity 47.4%; Pred. No. 13;

Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 KVDLTVKSGDAKTLVLN 20
:|||||:|:|:|:
Db 151 RIDLTVGKGTARTREINL 169

RESULT 11

ID Q8IHR4 PLAF7 PRELIMINARY; PRT; 837 AA.
AC Q8IHR4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DYNAMIN-like protein.
GN ORFNames=PF11_0465;
OS Plasmodium falciparum (isolate 3D7)
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]

NUCLEOTIDE SEQUENCE.

RP MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Fain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum";
RL Nature 419:498-511(2002).

DR EMBL: AE014843; AN36045.1; -: Genomic_DNA.
DR GO: GO:0005525; F:GTP binding; IEA.

DR GO: GO:0003924; F:GTPase activity; IEA.

DR InterPro: IPR001401; DYNAMIN.

DR InterPro: IPR000375; DYNAMIN_central.

DR InterPro: IPR003130; GED.

DR Pfam: PF01031; DYNAMIN_M; 1.

DR Pfam: PF00350; DYNAMIN_N; 1.

DR Pfam: PF02212; GED; 1.

DR PRINTS: PR00195; DYNAMIN.

SQ SEQUENCE 837 AA; 96373 MW; 42E0039489CFDDBC CRC64;

Query Match 52.1%; Score 49.5; DB 2; Length 837;
Best Local Similarity 52.6%; Pred. No. 40;
Matches 10; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 1 TKVDLTVKSGDAKTLVLN 19
:|||||:|:|:|:
Db 211 TKIDL-MDKGADASKMLLN 228

RESULT 12

ID Q8BJC6 PLAF7 PRELIMINARY; PRT; 837 AA.
AC Q8BJC6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DYNAMIN-like protein.
GN Name-dyn;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]

NUCLEOTIDE SEQUENCE.

RA Li H., Wu Y., Wang H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF336796; AAK26820.1; -: mRNA.
DR GO: GO:0005525; F:GTP binding; IEA.

DR GO: GO:0003924; F:GTPase activity; IEA.
DR InterPro: IPR001401; DYNAMIN.
DR InterPro: IPR000375; DYNAMIN_central.
DR InterPro: IPR003130; GED.
DR Pfam: PF01031; DYNAMIN_M; 1.
DR Pfam: PF00350; DYNAMIN_N; 1.
DR Pfam: PF02212; GED; 1.
DR PRINTS: PR00195; DYNAMIN.
DR SMART: SM00053; DYNC; 1.
DR SMART: SM00302; GED; 1.
KW GTP-binding; Nucleotide-binding.

SQ SEQUENCE 837 AA; 96374 MW; 42E0039489CFDDBC CRC64;

Query Match 52.1%; Score 49.5; DB 2; Length 837;
Best Local Similarity 52.6%; Pred. No. 40;
Matches 10; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 1 TKVDLTVKSGDAKTLVLN 19
:|||||:|:|:|:
Db 211 TKIDL-MDKGADASKMLLN 228

RESULT 13

ID RUVB_PROMM STANDARD; PRT; 352 AA.
AC Q7V910;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holliday junction DNA helicase RuvB.
GN Name=ruvB; OrderedLocusNames=PMT0156;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,

RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,

RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,

RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,

RA Webb E.A., Zinser E.R., Chisholm S.W.;

RT "Genome divergence in two Prochlorococcus ecotypes oceanic
niche differentiation";

RL Nature 424:1042-1047(2003).

CC -!- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures
cruciform structure in supercoiled DNA with palindromic sequence,
indicating that it may promote strand exchange reactions in

CC homologous recombination. RuvAB is an helicase that mediates the

CC Holliday junction migration by localized denaturation and

CC reannealing (By similarity).

CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).

CC -!- SIMILARITY: Belongs to the ruvB family.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: BX572095; CAE20331.1; -: Genomic_DNA.

DR HAMAP: MF 00016; -: 1.

DR InterPro: IPR003593; AAA_ATPase.

DR InterPro: IPR003959; AAA_ATPase_cent.

DR InterPro: IPR000767; Disease_resist.

DR InterPro: IPR004605; RuvB.

DR InterPro: IPR008823; RuvB_C.

DR InterPro: IPR008824; RuvB_N.

DR InterPro: IPR011991; Wing_hlx_DNA_bd.

DR Pfam: PF00004; AAA; 1.

DR Pfam: PF05491; RuvB_C; 1.

DR Pfam: PF05496; RuvB_N; 1.

```

DR PRINTS; PRO0364; DISEASERSIST.
DR SMART; SM00382; AAA; 1.
DR TIGRFAms; TIGR00635; ruvB; 1.
KW ATP-binding; Complete proteome; DNA damage; DNA recombination;
KW DNA repair; Helicase; Hydrolyase; Nucleotide-binding; SOS response.
FT NP_BIND 79 86 ATP [Potential].
SQ SEQUENCE 352 AA; 38109 MW; D66A32A321D35C67 CRC64;

Query Match 51.6%; Score 49; DB 1; Length 352;
Best Local Similarity 52.6%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLNI 20
Db 151 RLDTLVGKSGTARTRALEL 169

RESULT 14
Q4HIF6 9STRE
ID Q4HIF6_9STRE PRELIMINARY; PRT; 292 AA.
AC Q4HIF6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Nephritis-associated plasmin receptor (EC 1.2.1.12) (Fragment).
GN Name-naplr;
OS Streptococcus sp. K131.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=336390;
RN [1]_TaxID=336390;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K131;
RA Fujino M., Yamakami K., Oda T., Omasu F., Murai T., Yoshizawa N.;
RT "Nephritis-Associated Plasmin Receptor (NAPlr) in Acute
RT Poststreptococcal Glomerulonephritis: Nucleotide Sequence of Gene
RT Encoding NAPlr and Its Expression.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
EMBL; AB221042; BAE15968.1; -; Genomic_DNA.
KW Oxidoreductase; Receptor.
FT NON_TER 1
SQ SEQUENCE 292 AA; 31093 MW; 544C49C8BBD02F9 CRC64;

Query Match 50.5%; Score 48; DB 2; Length 292;
Best Local Similarity 55.8%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 19
Db 73 KVVITAPGSDVKTIIVEN 90

RESULT 15
Q9CDH4 LACLA
ID Q9CDH4_LACLA PRELIMINARY; PRT; 336 AA.
AC Q9CDH4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glyceroldehyde 3-phosphate dehydrogenase (EC 1.2.1.12).
GN Name-gapB; OrderedLocNames=LL2246;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]_TaxID=1360;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).

```

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CC -!- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
CC dehydrogenase family.
DR EMBL; AE006453; AAK06344.1; -; Genomic_DNA.
DR PIR; F86905; F86905.
DR HSSP; P00362; INQO.
DR GO; GO:0004365; F:Glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR GO; GO:0051287; F:NAD binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006006; P:glucose metabolism; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR006424; GAPDH-I.
DR InterPro; IPR000173; GAP_dhhydrogenase.
DR PANTHER; PTHR10836; GAP_dhhydrogenase; 1.
DR Pfam; PF02800; Gp_dh_C; 1.
DR Pfam; PF00044; Gp_dh_N; 1.
DR PRINTS; PR00078; G3PDHDEGNASE.
DR TIGRFAms; TIGR01534; GAPDH-I; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 336 AA; 35819 MW; 6C587383FCA2178B CRC64;

Query Match 50.5%; Score 48; DB 2; Length 336;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 19
Db 117 KVVITAPGSDVKTIIVEN 134

Search completed: February 16, 2006, 11:55:13
Job time : 52.2564 secs

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Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	95	100.0	97	2	A33422	allergen Lol pIII
2	59	62.1	118	2	T05550	pollen allergen ho
3	58	61.1	97	2	A34291	pollen allergen Lo
4	54	56.8	88	2	A48595	major allergen Lol
5	48	50.5	336	2	F86905	hypothetical prote
6	46	48.4	2658	2	F86216	protein t23G18.2 f
7	45	47.4	122	2	S39457	pollen allergen Ph
8	44	46.3	126	2	S63804	hypothetical prote
9	44	46.3	334	2	C69687	glyceraldehyde 3-p
10	44	46.3	334	2	S34254	glyceraldehyde 3-p
11	44	46.3	335	2	F95235	glyceraldehyde 3-p
12	44	46.3	336	2	A42963	glyceraldehyde 3-p
13	44	46.3	359	2	G98099	glyceraldehyde-3-p
14	43.5	45.8	240	2	T51484	CRSZ-like protein
15	43.5	45.8	808	1	T04982	dynamn-like prote
16	43	45.3	206	2	F64620	hypothetical prote
17	43	45.3	268	2	AH1646	hypothetical prote
18	43	45.3	299	2	T05494	glycine-rich prote
19	43	45.3	337	2	G86694	hypothetical prote
20	43	45.3	6642	2	T29757	protein UNC-89 - C
21	42.5	44.7	630	2	B64514	hypothetical prote
22	42	44.2	206	2	E71894	hypothetical prote
23	42	44.2	287	2	H69067	ATP phosphoribosyl
24	42	44.2	333	2	F90172	hypothetical prote
25	42	44.2	370	2	A41891	basal body P-ring
26	42	44.2	496	2	D83919	hypothetical prote
27	42	44.2	844	2	T32608	hypothetical prote
28	41	43.2	87	2	H96010	probable cell divi
29	41	43.2	180	2	AC0197	conserved hypothet

```

RESULT 3
A34291
pollen allergen Lol p IIA - perennial ryegrass
C:Species: Lolium perenne (perennial ryegrass)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C:Accession: A34291
R:Ansari, A.A.; Shenbagamurthi, P.; Marsh, D.G.
J. Biol. Chem. 264, 11181-11185, 1989
A:Title: Complete amino acid sequence of a Lolium perenne (perennial rye grass) pollen a
A:Reference number: A34291; MUID:89291864; PMID:2472390
A:Accession: A34291
A:Molecule type: protein
A:Residues: 1-97 <ANS>
A:Cross-references: UNIPROT:P14947; UNIPARC:UPI000012F496
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 61.1%; Score 58; DB 2; Length 97;
Best Local Similarity 56.7%; Pred. No. 0.025;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
|: ||||| | | | | |
DB 4 VFTVKGSDKKNLALSI 21

RESULT 4
A48595
major allergen Lol p II - perennial ryegrass (fragment)
C:Species: Lolium perenne (perennial ryegrass)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A48595
R:Sidoli, A.; Tamborini, E.; Giuntini, I.; Levi, S.; Volonte, G.; Painsi, C.; De Lalla, C.
J. Biol. Chem. 268, 21819-21825, 1993
A:Title: Cloning, expression, and immunological characterization of recombinant Lolium p
A:Reference number: A48595; MUID:94012768; PMID:7691817
A:Accession: A48595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-88 <STD>
A:Cross-references: UNIPROT:Q40239; UNIPARC:UPI000017999D
A:Experimental source: pollen
A:Note: sequence inconsistent with nucleotide translation
A:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 56.8%; Score 54; DB 2; Length 88;
Best Local Similarity 64.7%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 DLTVEKSGSDAKTLVLNI 20
: ||||| | | | | |
DB 1 EFTVKGSDKKNLALSI 17

RESULT 5
F86905
hypothetical protein gapB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86905
R:Bohlooin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <STO>
A:Cross-references: UNIPROT:Q9CDH4; UNIPARC:UPI000000C6COA; GB:AE005176; PID:g12725315; F

```

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: gapB

C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase

Query Match 50.5%; Score 48; DB 2; Length 336;

Best Local Similarity 55.6%; Pred. No. 4.3;

Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGSDAKTLVLNI 19

|: ||||| | | | | |

DB 117 KWTITAPGSDVKTIIVFN 134

RESULT 6

A86216

protein T23G18.2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: A86216

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.;

ansan, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86216

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2658 <STO>

A:Cross-references: UNIPROT:Q9SGE4; UNIPARC:UPI000009CA83; GB:AE005172; NID:g6579214; P1

C:Genetics:

A:Gene: T23G18.2

A:Map position: 1

Query Match 48.4%; Score 46; DB 2; Length 2658;

Best Local Similarity 55.6%; Pred. No. 84;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20

|: ||||| | | | | |

DB 950 VEETVNDGSDTSTLLLSI 967

RESULT 7

S39457

pollen allergen Phl p II - common timothy

C:Species: Phleum pratense (common timothy)

C:Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 31-Dec-2004

C:Accession: S39457

R:Dolecek, C.; Vrtala, S.; Laffer, S.; Steinberger, P.; Kraft, D.; Scheiner, O.; Valent;

FEMS Lett. 335, 299-304, 1993

A:Title: Molecular characterization of Phl p II, a major timothy grass (Phleum pratense

A:Reference number: S39457; MUID:94085541; PMID:8262175

A:Accession: S39457

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-122 <DOL>

A:Cross-references: UNIPROT:P43214; UNIPARC:UPI0000000331; EMBL:X75925; NID:g415895; P1

C:Superfamily: Pollen allergen, Group II

C:Keywords: pollen

Query Match 47.4%; Score 45; DB 2; Length 122;

Best Local Similarity 58.8%; Pred. No. 4.5;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGSDAKTLVL 18

|: ||||| | | | | |

Db 29 KVTFTVEKGSNEKHLAV 45

RESULT 8

hypothesis:

C: Date:

R. T. Osgood

MOI: MIC
8: Tit + 10

A; refer

A;Status

A;Residue

A;Note: t

Query N

Method

.

RESULT 9

2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 2681, 26

...spectra

C; Accessi

.; Daly,

A;Title:

A: Accessi

A; Statu

A; Residue

A: Experiment

Genetic

C; Superfa

Query M

Matches

2

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•
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•

S34254

Species:

Date: 2/

R; Oster,

A: Descrip

A: Accoppi

A; MOLECUL

A; Cross-r

Qy	2	KVDLTVEKGSDA-KTLVLN	19
		::: : :	
Dh	202	OIEALEOGSEAVKTLVLN	220

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 11:57:35 ; Search time 3.58974 Seconds
(without alignments)
79.196 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95

Sequence: 1 TKVDLTVEKGSDAKTLVLNI 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New*

- 1: /cgn2_6/prodata/1/pubpa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/prodata/1/pubpa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/1/pubpa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/1/pubpa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/1/pubpa/US05_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/1/pubpa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/1/pubpa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/1/pubpa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	97	6	US-10-498-026-33
2	58	61.1	97	6	US-10-498-026-32
3	45	47.4	122	6	US-10-498-026-47
4	43	45.3	201	7	US-11-082-389-112
5	41	43.2	35	7	US-11-233-683-54
6	41	43.2	262	6	US-10-498-026-46
7	41	43.2	263	6	US-10-498-026-45
8	41	43.2	263	7	US-11-033-039-193
9	41	43.2	373	6	US-10-793-626-372
10	40	42.1	379	7	US-11-098-686-10989
11	39	41.1	189	6	US-10-454-437-378
12	39	41.1	325	6	US-10-467-657-14
13	39	41.1	325	6	US-10-467-657-5568
14	39	41.1	467	6	US-10-467-657-2612
15	39	41.1	1360	7	US-11-241-056-14
16	38.5	40.5	295	7	US-11-169-041-139
17	38.5	40.5	295	7	US-11-072-175-146
18	38.5	40.5	719	6	US-10-505-263-87
19	38	40.0	35	7	US-11-233-683-49
20	38	40.0	184	6	US-10-131-826A-76
21	38	40.0	252	7	US-11-098-686-10112
22	38	40.0	323	7	US-11-098-686-11288
23	38	40.0	354	7	US-11-108-528-50
24	38	40.0	478	6	US-10-467-657-3994
25	38	40.0	879	7	US-11-098-686-10290

26	38	40.0	1613	7	US-11-108-528-84	Sequence 84, Appl
27	38	40.0	1613	7	US-11-108-528-86	Sequence 86, Appl
28	37.5	39.5	304	6	US-10-793-626-2190	Sequence 2190, Ap
29	37.5	39.5	555	7	US-11-124-368A-300	Sequence 300, App
30	37.5	39.5	749	7	US-11-124-368A-299	Sequence 299, App
31	37.5	39.5	859	7	US-11-124-368A-298	Sequence 298, App
32	37.5	39.5	877	7	US-11-124-368A-302	Sequence 302, App
33	37	38.9	141	6	US-10-793-626-2886	Sequence 2886, Ap
34	37	38.9	141	6	US-10-793-626-3084	Sequence 3084, Ap
35	37	38.9	304	7	US-11-152-569-11	Sequence 11, Appl
36	37	38.9	316	6	US-10-467-657-8092	Sequence 8092, Ap
37	37	38.9	425	7	US-11-055-822-1104	Sequence 1104, Ap
38	37	38.9	687	7	US-11-185-342-16	Sequence 16, Appl
39	37	38.9	687	7	US-11-185-560-4	Sequence 4, Appl
40	37	38.9	792	6	US-10-467-657-6026	Sequence 6026, Ap
41	37	38.9	792	6	US-10-467-657-7528	Sequence 7528, Ap
42	37	38.9	792	7	US-11-103-957-92	Sequence 92, Appl
43	37	38.9	1637	6	US-10-821-234-1204	Sequence 1204, Ap
44	36	37.9	333	7	US-11-216-267-30	Sequence 30, Appl
45	36	37.9	333	7	US-11-232-382-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-498-026-33
; Sequence 33, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-33

Query Match 100.0%; Score 95; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
DB 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 2
US-10-498-026-32
; Sequence 32, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-32

Query Match 61.1%; Score 58; DB 6; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.0051;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-112

Query Match      45.3%; Score 43; DB 7; Length 201;
Best Local Similarity 45.0%; Pred. No. 3.9;
Matches 9; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLI 20
   : : : : : ||| : : : : : |||
Db 6 SNLNLTVADGSTSRLLANNI 25

RESULT 5
US-11-233-683-54
; Sequence 54, Application US/112333683
; Publication No. US20060025573A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/11/233,683
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: modified IgG2CH1-IgG1hinge fusion junction
US-11-233-683-54

Query Match      43.2%; Score 41; DB 7; Length 35;
Best Local Similarity 66.7%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKT 15
   ||| ||| ||| |||
Db 14 TKVDKTVPEKGSDDKT 28

RESULT 6
US-10-498-026-46
; Sequence 46, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Phleum pratense
US-10-498-026-46

Query Match      43.2%; Score 41; DB 6; Length 262;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVL 18
   ||| ||| ||| |||
Db 168 TKVTFVEKGSNPNYLAL 185

RESULT 7
US-10-498-026-45
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-112

Query Match      47.4%; Score 45; DB 6; Length 122;
Best Local Similarity 58.8%; Pred. No. 0.99;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVL 18
   ||| ||| ||| |||
Db 29 KVTFTVEKGSNEKHLAV 45

RESULT 4
US-11-082-389-112
; Sequence 112, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BG1-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 112
; LENGTH: 201
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; Sequence 45, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Phleum pratense
; US-10-498-026-45

Query Match 43.2%; Score 41; DB 6; Length 263;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVL 18
||| |||||:
Db 168 TKVTFHVEKGSNPYLAL 185

RESULT 8

; US-11-033-039-193
; Sequence 193, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 193
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Phleum pratense
; US-11-033-039-193

Query Match 43.2%; Score 41; DB 7; Length 263;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVL 18
||| |||||:
Db 168 TKVTFHVEKGSNPYLAL 185

RESULT 9

; US-10-793-626-372
; Sequence 372, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 372
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-372

Query Match 43.2%; Score 41; DB 6; Length 373;
Best Local Similarity 52.4%; Pred. No. 18;
Matches 11; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 5 LTVEKGSDAKTL-----VLN 19
:|||||:|:
Db 197 VTVEKGSDDKDVGGKVKVLN 217

RESULT 10

; US-11-098-686-10989
; Sequence 10989, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10989
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-10989

Query Match 42.1%; Score 40; DB 7; Length 379;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTL 16
|:::|||:|:
Db 117 TELDVTVSSVGDAKSL 132

RESULT 11

; US-10-454-437-378
; Sequence 378, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09

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; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 378
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-378

Query Match          41.1%; Score 39; DB 6; Length 189;
Best Local Similarity 35.3%; Pred. No. 17;
Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLN 19
Db 153 IESSINKGEDNKILLVD 169

RESULT 12
US-10-467-657-14
; Sequence 14, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 14
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-14

Query Match          41.1%; Score 39; DB 6; Length 325;
Best Local Similarity 57.1%; Pred. No. 33;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LTVKSGSDAKTLVL 18
Db 286 LTVKSGSEVKNEIL 299

RESULT 13
US-10-467-657-5568
; Sequence 5568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5568
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5568

Query Match          41.1%; Score 39; DB 6; Length 325;
Best Local Similarity 57.1%; Pred. No. 33;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LTVKSGSDAKTLVL 18
Db 286 LTVKSGSEVKNEIL 299

RESULT 14
US-10-467-657-2612
; Sequence 2612, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2612
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2612

Query Match          41.1%; Score 39; DB 6; Length 467;
Best Local Similarity 35.3%; Pred. No. 52;
Matches 6; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLN 19
Db 67 IDIALERTSLRTAVLN 83

RESULT 15
US-11-241-056-14
; Sequence 14, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 14
; LENGTH: 1360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-241-056-14

Query Match 41.1%; Score 39; DB 7; Length 1360;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVEKGSDAKTL 16
Db 1195 VDLTVEEGQRLKVI 1208

Search completed: February 16, 2006, 12:01:47
Job time : 3.58974 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:55:30 ; Search time 11.453 Seconds
(without alignments)
144.374 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95
Sequence: 1 TKVDLTVKGSDAKTLVNI 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/aaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/aaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/aaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	30	1 US-08-433-854-9	Sequence 9, Appli
2	95	100.0	30	1 US-08-174-745A-9	Sequence 9, Appli
3	95	100.0	30	1 US-08-195-947-9	Sequence 9, Appli
4	95	100.0	30	1 US-08-433-885-9	Sequence 9, Appli
5	95	100.0	30	1 US-08-433-908B-9	Sequence 9, Appli
6	95	100.0	30	2 US-08-410-614-9	Sequence 9, Appli
7	95	100.0	31	2 US-08-413-974-25	Sequence 25, Appl
8	95	100.0	31	2 US-08-434-418-25	Sequence 25, Appl
9	95	100.0	31	2 US-08-433-288-25	Sequence 25, Appl
10	95	100.0	31	2 US-08-174-739A-25	Sequence 25, Appl
11	95	100.0	31	2 US-08-434-256-25	Sequence 25, Appl
12	58	61.1	31	1 US-08-433-854-8	Sequence 8, Appli
13	58	61.1	31	1 US-08-174-745A-8	Sequence 8, Appli
14	58	61.1	31	1 US-08-195-947-8	Sequence 8, Appli
15	58	61.1	31	1 US-08-433-885-8	Sequence 8, Appli
16	58	61.1	31	1 US-08-433-908B-8	Sequence 8, Appli
17	58	61.1	31	1 US-08-413-974-23	Sequence 23, Appl
18	58	61.1	31	2 US-08-413-974-24	Sequence 24, Appl
19	58	61.1	31	2 US-08-434-418-23	Sequence 23, Appl
20	58	61.1	31	2 US-08-433-288-23	Sequence 23, Appl
21	58	61.1	31	2 US-08-174-739A-23	Sequence 23, Appl
22	58	61.1	31	2 US-08-174-739A-24	Sequence 24, Appl
23	58	61.1	31	2 US-08-410-614-8	Sequence 8, Appli
24	58	61.1	31	2 US-08-434-256-23	Sequence 23, Appl
25	58	61.1	31	2 US-08-434-256-24	Sequence 24, Appl
26	47	49.5	639	2 US-08-270-767-45908	Sequence 45908, A
27	44	46.3	333	2 US-08-961-083-54	Sequence 54, Appl

28	44	46.3	333	2	US-09-536-784-54	Sequence 54, Appli
29	44	46.3	333	2	US-09-765-271-54	Sequence 54, Appli
30	44	46.3	333	2	US-09-765-272A-54	Sequence 54, Appli
31	44	46.3	335	2	US-09-878-781-14	Sequence 14, Appli
32	44	46.3	336	1	US-07-928-462-2	Sequence 2, Appli
33	44	46.3	336	2	US-08-273-247-2	Sequence 2, Appli
34	44	46.3	336	2	US-09-878-766A-12	Sequence 12, Appli
35	44	46.3	336	2	US-09-878-766A-14	Sequence 14, Appli
36	44	46.3	336	2	US-10-134-297-4	Sequence 4, Appli
37	44	46.3	336	2	US-10-134-297-6	Sequence 6, Appli
38	44	46.3	336	2	US-09-878-781-4	Sequence 4, Appli
39	44	46.3	336	2	US-09-878-781-6	Sequence 6, Appli
40	44	46.3	336	2	US-10-650-369-12	Sequence 12, Appli
41	44	46.3	336	2	US-10-650-369-14	Sequence 14, Appli
42	44	46.3	359	2	US-09-583-110-4722	Sequence 4722, Ap
43	44	46.3	369	2	US-09-107-433-2790	Sequence 2790, Ap
44	44	46.3	448	2	US-09-878-766A-22	Sequence 22, Appli
45	44	46.3	448	2	US-10-650-369-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-08-433-854-9
; Sequence 9, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjologlu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-9

Query Match 100.0% Score 95; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 2

US-08-174-745A-9
; Sequence 9, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphiglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-174-745A-9

Query Match 100.0%; Score 95; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 3

US-08-195-947-9
; Sequence 9, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.

; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphiglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-195-947-9

Query Match 100.0%; Score 95; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 4

US-08-433-885-9
; Sequence 9, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphiglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-885-9
;
; Query Match 100.0%; Score 95; DB 1; Length 30;
; Best Local Similarity 100.0%; Pred. No. 1.1e-09;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20
;
; RESULT 5
; US-08-433-908B-9
; Sequence 9, Application US/08433908B
; Patent No. 5965455
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,908B
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D4
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-908B-9
;
; Query Match 100.0%; Score 95; DB 1; Length 30;
; Best Local Similarity 100.0%; Pred. No. 1.1e-09;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20
;
; RESULT 6
; US-08-410-614-9
; Sequence 9, Application US/08410614
; Patent No. 6277383
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/195,947
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-410-614-9
;
; Query Match 100.0%; Score 95; DB 2; Length 30;
; Best Local Similarity 100.0%; Pred. No. 1.1e-09;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20
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RESULT 7
US-08-413-974-25
; Sequence 25, Application US/08413974
; Patent No. 6180368
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180368ris
; STREET: 1 Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,974
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,861
; FILING DATE:
; APPLICATION NUMBER: US/07/746,703
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3949
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-413-974-25

Query Match 100.0%; Score 95; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 2 TKVDLTVEKGSDAKTLVLNI 21

RESULT 8
US-08-434-418-25
; Sequence 25, Application US/08434418
; Patent No. 6197313
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir et al.
; TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
; FILE REFERENCE: IMI-051CND2
; CURRENT APPLICATION NUMBER: US/08/434,418
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 08/202,861
; PRIOR FILING DATE: 1994-25-02
; NUMBER OF SEQ ID NOS: 25

Query Match 100.0%; Score 95; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 2 TKVDLTVEKGSDAKTLVLNI 21

RESULT 9
US-08-433-288-25
; Sequence 25, Application US/08433288
; Patent No. 6239269
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir et al.
; TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
; FILE REFERENCE: IMI-051CND1
; CURRENT APPLICATION NUMBER: US/08/433,288
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 08/413,947
; PRIOR FILING DATE: 1995-03-30
; PRIOR APPLICATION NUMBER: 08/202,861
; PRIOR FILING DATE: 1994-02-25
; PRIOR APPLICATION NUMBER: 07/746,703
; PRIOR FILING DATE: 1991-08-16
; PRIOR APPLICATION NUMBER: 07/585,086
; PRIOR FILING DATE: 1990-10-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Lolium perenne
; FEATURE:
; OTHER INFORMATION: all occurrences of Xaa = any amino acid
; US-08-433-288-25

Query Match 100.0%; Score 95; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 2 TKVDLTVEKGSDAKTLVLNI 21

RESULT 10
US-08-174-739A-25
; Sequence 25, Application US/08174739A
; Patent No. 6265566
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lahive & Cockfield, LLP
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
```


;; GENERAL INFORMATION:
;; APPLICANT: Singh, Mohan Bir
;; APPLICANT: Knox, Robert B.
;; APPLICANT: Smith, Penelope
;; APPLICANT: Avjioğlu, Asil
;; APPLICANT: Theerakulpisut, Piyada
;; APPLICANT: Hough, Terryn
;; APPLICANT: Suphioglu, Cenik
;; APPLICANT: Ong, Eng Kok
;; TITLE OF INVENTION: Ryegrass Pollen Allergen
;; NUMBER OF SEQUENCES: 53
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362rls
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/174,745A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/930,060
;; FILING DATE: 14-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hohenschutz, Liza D.
;; REGISTRATION NUMBER: 33,712
;; REFERENCE/DOCKET NUMBER: IMPH-0024
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-174-745A-8
Query Match 61.1%; Score 58; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 0.0033;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 VDLTVKSGSDAKTLVLI 20
|:|||||||:|:
Db 4 VEFTVEKSGDEKNLALS 21
RESULT 14
US-08-195-947-8
; Sequence 8, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjioğlu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/195,947
;; FILING DATE: 14-FEB-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/930,060
;; FILING DATE: 14-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hohenschutz, Liza D.
;; REGISTRATION NUMBER: 33,712
;; REFERENCE/DOCKET NUMBER: IMPH-0024
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-195-947-8
Query Match 61.1%; Score 58; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 0.0033;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 VDLTVKSGSDAKTLVLI 20
|:|||||||:|:
Db 4 VEFTVEKSGDEKNLALS 21
RESULT 15
US-08-433-885-8
; Sequence 8, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjioğlu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield.
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy B.
; REGISTRATION NUMBER: 36,207

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; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-885-8

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Query Match      61.1%; Score 58; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. NO. 0.0033;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      3 VDLTVEKGSDAKTLVNI 20
      |: ||||| | | | |
Db      4 VEFTVEKGSDEKNLALSI 21

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Search completed: February 16, 2006, 11:57:17
Job time : 11.453 secs

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